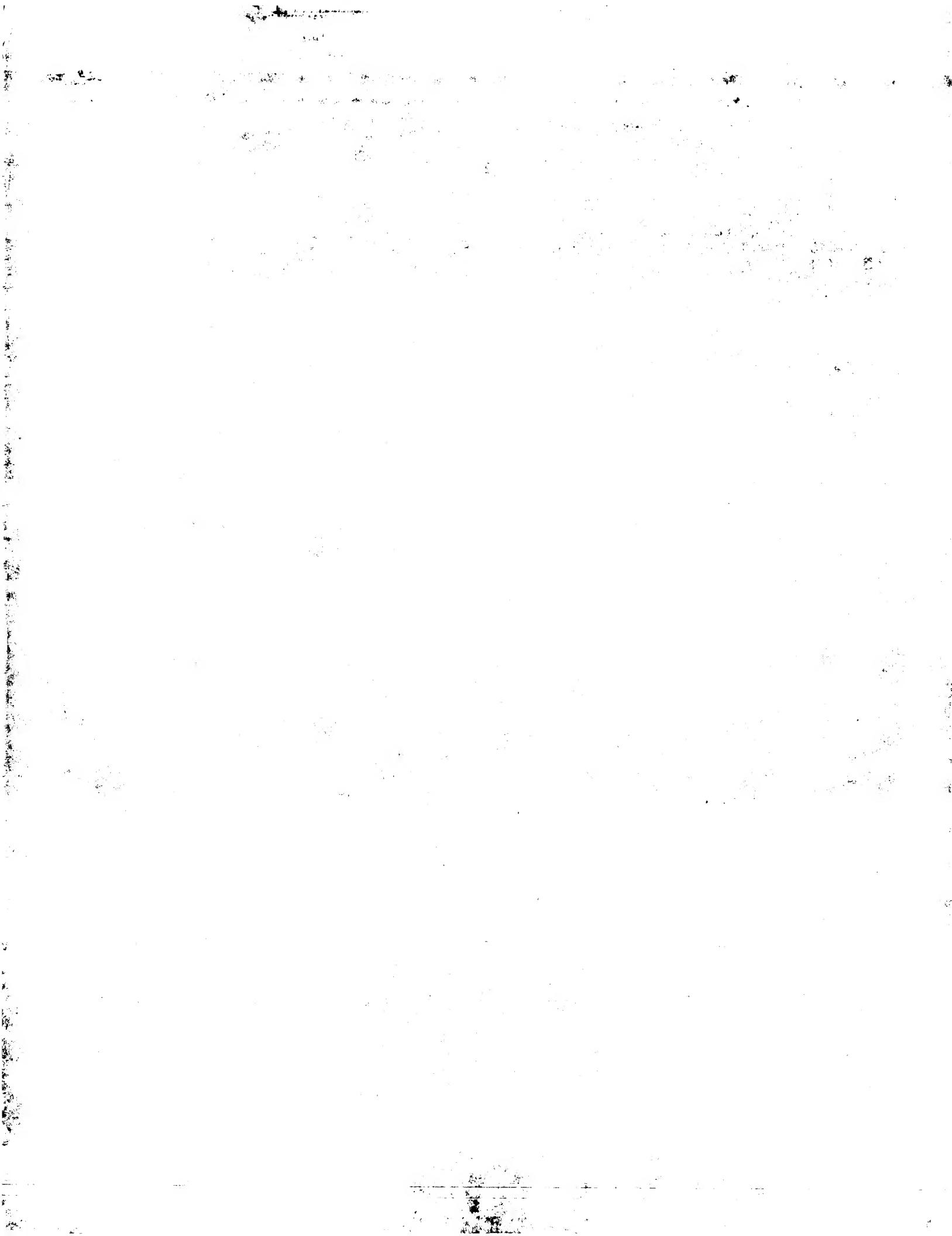


Yu, Misook

To: STIC-Biotech/ChemLib
Subject: 09847102

Please search SEQ ID NO:68 and DNA encoding SEQ ID NO:68.

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)



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OM protein - protein search, using SW model

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 9084700

Maximum DB seq length: 200000000

Maximum Match 100%
Listing first 45 summarise

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Database : A_Geneseq_101002:  
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10: /SIDS2/gcdata/geneseq/geneseq - emb1/AA1999.DAT:*
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21: /SIDSB/gcadata/geneseq/geneseq-emb1/AA2009.DAT;
22: /SIDSB/gcadata/geneseq/geneseq-emb1/AA2001.DAT;
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

SUMMARIES

NO.	Score	Query	Match	Length	DB	ID	Description
-----	-------	-------	-------	--------	----	----	-------------

1	1310	100.0	585	18	AAW3127/1			
2	824	62.9	694	18	AAU74823			
3	823.5	62.9	685	18	AAW31274			
						Human	Intr	
						RE		
						Mouse	FRI	

5	62.1	47.4	69.4	22	AB51797
6	44.0	33.6	57.2	18	AAW1273
7	41.5	31.7	64.7	21	AB12117
8	38.4	29.3	58.1	22	AA573308
9	38.0	29.0	32.5	19	AAW1767
10	37.2	28.4	32.5	19	AAW8695

ALIGNMENTS

19: /SIS2/gggdatt/geneseq/geneseqp-emb1/AA1998 DAT: * DB: Human frizzled-5 protein Mfz25 (Wnt-receptor)..
 20: /SIS2/gggdatt/geneseq/geneseqp-emb1/AA1999 DAT: * XX
 21: /SIS2/gggdatt/geneseq/geneseqp-emb1/AA2000 DAT: * KW Wnt receptor; human frizzled-5 protein; Mfz25 gene;
 22: /SIS2/gggdatt/geneseq/geneseqp-emb1/AA2001 DAT: * signal transduction; cancer; cell growth; cell proliferation;
 23: /SIS2/gggdatt/geneseq/geneseqp-emb1/AA2002 DAT: * KW

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

PT treatment of cancer and growth, development or proliferation related disorders
 PT 21-TUN-2000; 2000US-21402P.
 XX 25-AUG-2000; 2000US-228045P.
 PS Disclosure; Page 37-39; 61pp; English.
 XX PR 12-BCC-2000; 2000US-255104P.
 PA (INCY-) INCYTE GENOMICS INC.
 XX PR Griffin JA, Kalllick DA, Tribouley CM, Yue H, Nguyen DB, Tang YT;
 PI Dal P, Policky JL, Azimzai Y, Lu DAW, Graul R, Yao MG, Burford N;
 CC Hafflin AJA, Baughn MR, Bandman O, Patterson C, Yang J, Xu Y;
 CC Gandhi AR, Warren BA, Ding L, Sanjanwala MS, Duggan BM, Lu Y;
 CC DR WPI; 2002-090432/12.
 CC N-PSDB; ABK15174.
 XX PR
 CC This invention relates to a Wnt receptor, encoded by the *Hfz5* gene (see AAH8989). It is an example of a Wnt receptor. Other novel frizzled family members have been identified in human, mouse and *Caenorhabditis elegans* (see AAW31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.

SQ Sequence 585 AA;

Query Match 100.0%; Score 1310; DB 18; Length 585;
 Best Local Similarity 100.0%; Pred. No. 8.6e-102; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPPSAPSPLILLILQLAQVGRAAAASKAVPCVQEIYTVPGRGIGYNLTIMPQNPHDQ 60
 Db 1 MARPPSAPSPLILLILQLAQVGRAAAASKAVPCVQEIYTVPGRGIGYNLTIMPQNPHDQ 60
 QY 61 DEAGLEHVQFPLVLSIQCSDLRFLCTMTPICPDYHKLPLPPRSVCERAKAGCSPLM 120
 Db 61 DEAGLEHVQFPLVLSIQCSDLRFLCTMTPICPDYHKLPLPPRSVCERAKAGCSPLM 120
 QY 121 ROYGAWPERMSCDRLPVGLGRDAEVLQMDNTNSEATTAPPRPFPAKTRPGPPGAPASGG 180
 Db 121 ROYGAWPERMSCDRLPVGLGRDAEVLQMDNTNSEATTAPPRPFPAKTRPGPPGAPASGG 180
 QY 181 ECPAGGPFVCKCREPFVPIKESHLINKYKRTGOVNCAPCYOQSFSADERTF 235
 Db 181 ECPAGGPFVCKCREPFVPIKESHLINKYKRTGOVNCAPCYOQSFSADERTF 235

RESULT 2
 AAU74823
 ID AAU74823 standard; protein; 694 AA.
 XX
 AC AAU74823;
 DT 23-APR-2002 (first entry)
 DE Human REPTR 6 protein.

SQ Sequence 694 AA;

Query Match 62.9%; Score 824; DB 23; Length 694;
 Best Local Similarity 59.9%; Pred. No. 6.6e-61; Mismatches 39; Indels 48; Gaps 8;

XX Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;
 KW Human REPTR 6 protein.
 KW REPTR; human; antiinflammatory; cytostatic; immunosuppressive; antiviral; anti-HIV; antiarthritic; anticonvulsant; nootropic; neuroprotective; antiallergic; antibody; immunogen; endometriosis; autoimmune disease; irritable bowel syndrome; ulcerative colitis; Crohn's disease; endocrine disorder; hypothalamic disorder; Kallman's disease; autoimmune disease; inflammatory disease; infertility; receptor; acquired immune deficiency syndrome; AIDS; rheumatoid arthritis; allergy; osteoarthritis; diabetes mellitus; multiple sclerosis; systemic lupus erythematosus; cell proliferative disorder; cancer; developmental disorder; Duchenne muscular dystrophy; Becker muscular dystrophy; neurological disorder; epilepsy; Alzheimer's disease; Huntington's disease; reproductive disorder. Homo sapiens.

XX WO200198354-A2.

XX 27-DEC-2001.

XX 21-JUN-2001; 2001WO-US19942.

XX PR
 XX 21-TUN-2000; 2000US-21402P.
 XX 25-AUG-2000; 2000US-228045P.
 XX 12-BCC-2000; 2000US-255104P.
 XX PR
 XX (INCY-) INCYTE GENOMICS INC.
 XX PR Griffin JA, Kalllick DA, Tribouley CM, Yue H, Nguyen DB, Tang YT;
 PI Dal P, Policky JL, Azimzai Y, Lu DAW, Graul R, Yao MG, Burford N;
 CC Hafflin AJA, Baughn MR, Bandman O, Patterson C, Yang J, Xu Y;
 CC Gandhi AR, Warren BA, Ding L, Sanjanwala MS, Duggan BM, Lu Y;
 CC DR WPI; 2002-090432/12.
 XX PR
 CC This invention relates to twelve human receptors cDNA sequences referred to as REPR-1 to REPR-12, and the proteins encoded thereby. The proteins of the invention may have antiinflammatory, cytotoxic, immunosuppressive, antiviral, anti-HIV, antiarrhythmic, muscular active general, anticonvulsant, nootropic, neuroprotective, antiallergic activities. The sequences of the invention may be used to produce REPR agonists or antagonists, and the protein sequences may be used to raise anti-REPR antibodies. These molecules and the REPR polynucleotides and polypeptides of the invention are useful in the diagnosis, treatment and prevention of gastrointestinal (e.g. gastritis, oesophageal carcinoma, Crohn's disease, irritable bowel syndrome, ulcerative colitis), autoimmune (e.g. hypothyroidism disorder, Kallman's disease), autoimmunity/rheumatoid arthritis, allergies, osteoarthritis, diabetes mellitus, multiple sclerosis, systemic lupus erythematosus, cell proliferative (e.g. cancer), developmental (e.g. Duchenne and Becker muscular dystrophy), neurological (e.g. epilepsy, Alzheimer's disease, Huntington's disease) and reproductive (e.g. infertility, endometriosis) disorders. Numerous other examples of each disorder are given in the specification. The present sequence represents the human REPR6 protein sequence of the invention.

XX SQ Sequence 694 AA;

Query Match 11 SLL--LILLAQLQVGRAAAASKAVPCVQEIYTVPGRGIGYNLTIMPQNPHDQDEAGLEVH 68
 Db 11 SLLAALLQLQRSSGAAASAKELACOEBITVPLCKGIGNYTMQPNPHDQDEAGLEVH 70
 QY 69 QFWPLVLEQCSPLDRFLCTMTPICPDYHKLPLPPRSVCERAKAGCSPLMQYKAWP 128
 Db 71 QFWPLVLEQCSPLDRFLCTMTPICPDYHKLPLPPRSVCERAKAGCSPLMQYKAWP 130
 QY 129 ERMSCDRLPVGLGRDAEVLQMDNTNSEATT---PPRPFPAKTRPLPG-----PPG 174
 Db 131 DRMSCDRLPEQG-NPDTLQCMDNTDLTTAASPRLPPP--PGQOPPSSSGHGRPPG 187
 QY 175 A-----PASGG-----SCPAGGFV---CKREPFVPIKESHP 205
 Db 188 ARPPHRGGRRGGGGDAAPPARGGGGKARPPGGGAAPCSPGCQCRAPMYSVSSRHP 247
 QY 206 LNKYKRTGOVNCAPCYOQSFSADERTF 234
 Db 248 LYNRVKTQIANCALPCNHPFSQDERAF 276

RESULT 3
 ID AAU1274 standard; Protein; 685 AA.

XX
AC AAM31274;
XX DT 27-APR-1998 (first entry)
XX DE Mouse frizzled-8 protein Mfz8 (Wnt receptor).
XX KW Wnt receptor; mouse frizzled-8 protein; Mfz8 gene;
XX signal transduction; cancer; cell growth; cell proliferation.
OS Mus musculus.
XX PN WO9739357-A1.
XX PD 23-OCT-1997.
XX PP 11-APR-1997; 97WO-US06049.
XX PR 12-APR-1996; 96US-0015307.
XX PA (UYJO) UNIV JOHNS HOPKINS.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX PT Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J;
PT Nusse R, Samos CH, Wangy;
XX WPI; 1997-526631/48.
DR N-PSDB; AAT89892.
XX PT Identification of Wnt receptor binding modulators - useful for
PT treatment of cancer and growth, development or proliferation related
PT disorders
XX PS Disclosure; Page 48-50; 61pp; English.
XX CC This protein comprises the mouse transmembrane receptor,
CC frizzled-8 (Mfz8), encoded by the Mfz8 gene (see AAT89892). It is
CC an example of a Wnt receptor. Other novel frizzled family members
CC have been identified in human, mouse and *Caenorhabditis elegans*
(see AAW11268-74) and are considered also to be Wnt receptors. Wnt
CC receptors can be used in a novel claimed method of screening for
CC compounds which modulate the binding of a Wnt polypeptide (secreted
CC proteins involved in cell-to-cell signalling) to a Wnt receptor.
CC Wnt is involved in (mammary) cancer and other processes involving
CC growth, development and proliferation (both normal and abnormal).
CC Modulators identified by the claimed method are useful for
CC treatment of diseases related to these conditions.
XX SQ Sequence 685 AA;

Query Match 62.9%; Score 823.5; DB 18; length 685;
Best local Similarity 60.0%; Pred. No. 7.2e-61;
Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;

QY 11 SLU-LLUQAQLVGRAAASKAPVQOBETVPMERGIGNLTHPNQFNHDTOEAGLVEH 68
Db 11 SLLAALAVIQLQRSSGAAANSAKELACQETIVPLCKIGIGNTYMPNQFNHDTOEAGLVEH 70
QY 69 QFPILVEQCSPLRFLFCTMYPICLDPYKLPUPCSCVCEAKAGSPLRQYGRAMP 128
Db 71 QFWPLVLEIQCSPDILKFFLCMSMTPICLSDYKPKLUPCSCVCEAKASCAPLMLROYGRAMP 130
QY 129 ERNSCDRDLPEVLGRDAEVLCMDTNRSEATA---PPRPFPKAPETLPG-----PPG 174
Db 131 DRNRCDRDLPEQG-NPDTLMDYNTDLTAAPSPRRLLPPPP-PGQPPSGSGHSRPPG 188
QY 175 A-----PASEGEC--PAGGGFV---CKCRBPFVPLKSHPLNK 209
Db 189 ARPPHRGGSRGSDAAAPPSSRGKARPPGGGAACPEGCCOCRAPMVSSSBRHPLYN 248
QY 210 VRGCPVPCAVPCVQCPSSADEFV 234
Db 249 VKTGQIANCALPCHNPFFSODERA 273

RESULT 4
ID AAM31267
ID AAM31267 standard; Protein; 694 AA.
XX AC AAM31267;
XX DT 27-APR-1998 (first entry)
XX DE Drosophila frizzled-2 protein (Wnt receptor).
XX KW Wnt receptor; *Drosophila frizzled-2 protein*; *Dfz2* gene;
KW wingless receptor; *Wg* receptor; Signal transduction; Cancer;
KW cell growth; cell proliferation.
OS Drosophila melanogaster.
XX FH Key Location/Qualifiers
FT Misc-difference 268 /note= "encoded by CAC"
FT Misc-difference 269 /note= "encoded by TCG"
FT Misc-difference 348 /note= "encoded by TA (apparent: 1 nucleotide
FT deletion of codon)"
FT Misc-difference 488 /note= "encoded by TTA"
FT Misc-difference 632 /note= "encoded by CTG"
FT Misc-difference 633 /note= "encoded by GCG"
FT Misc-difference 671 /note= "encoded by CGC"
FT /note= "encoded by CG (apparent: 1 nucleotide
FT deletion of codon)"
XX PN WO9739357-A1.
XX PD 23-OCT-1997.
XX PR 11-APR-1997; 97WO-US06049.
XX PA (UYJO) UNIV JOHNS HOPKINS.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX PT Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J;
PT Nusse R, Samos CH, Wangy;
XX WPI; 1997-526631/48.
DR N-PSDB; AAT89885.
XX PT Identification of Wnt receptor binding modulators - useful for
PT treatment of cancer and growth, development or proliferation related
PT disorders
XX PS Claim 2; Page 23-25; 61pp; English.
XX CC This protein comprises the *Drosophila* frizzled-2 protein encoded by
the *Dfz2* gene (see AAT89892). It is a receptor for wingless (*Wg*),
CC acting as a signal transducing molecule, and is an example of a Wnt
receptor (*WntR*). Other novel frizzled family members have been
CC identified in human, mouse and *Caenorhabditis elegans* (see
AAW11268-74) and are considered also to be Wnt receptors. Wnt
CC receptors can be used in a novel, claimed method of screening for
CC compounds which modulate the binding of a Wnt polypeptide (secreted
CC proteins involved in cell-to-cell signalling) to a Wnt receptor.
CC Wnt is involved in (mammary) cancer and other processes involving
CC growth, development and proliferation (both normal and abnormal).
CC Modulators identified by the claimed method are useful for
CC treatment of diseases related to these conditions.

Sequence	694 AA;	Score 47.4%;	Score 621; DB 18;	Length 694;
Best Local Similarity	43.4%;	Pred.	No. 7.3e-44;	
Matches	124;	Conservative	27;	Mismatches 55;
Indels	80;	Gap		
OY	22 GRAAAASKPA-----VCOBIVTMPCRGIGYNLTHMPNOFNHDTOBAGLEVH 6			
Db	40 GHLGLDASAPPGVPAIPKPDNLRCRBEITTCMCRGIGYNNMFSFPNEMNHETDEAGLEHV 9			
OY	69 QFWMPUYEIQCOPDLRFLCTMTTPICLDPYHKKPLPCCRSTCERAKAGCSLMRQGFAMP 1			
Db	160 ERMACBHLPLHG-DPDNLCKMBQPSYTEAGSGGSSGGSGSGKRGKQGSGSGGS 2			
OY	151 ----NNESEATTAAPPREPPPAKOTLTLPSPGAGAASGGCPAGGPPFVCKCREPPV----- 1			
Db	219 GAGGSSGSTTKPCGRNSK-NCONPOGEKAKGSKCS----GCSRSPFLGKEQLLQ 235			
OY	198 ----PILKESHPLYKV--RTGQVNPNCAVPCYQPSFSADERTPA 317			
Db	272 QOSQMPMMHHPHWWMNLTVTORYASVNPNCIPCKPKPFSSIDEKFA 317			
RESULT 5				
ID	ABB71797	standard; Protein:	694 AA.	
XX				
AC	ABB71797;			
XX				
DT	26-MAR-2002	(first entry)		
DE	Drosophila melanogaster	polypeptide SEQ ID NO 42183.		
XX				
KW	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.			
XX				
OS	Drosophila melanogaster.			
XX				
PN	WO200171042-A2.			
XX				
PD	27-SEP-2001.			
XX				
PF	23-MAR-2001; 2001WO-US09231.			
XX				
PR	23-MAR-2000; 2000US-191637P.			
XX				
PR	11-JUL-2000; 2000US-0614150.			
XX				
PA	(PEKE) PE CORP NY.			
XX				
PT	Venter JC, Adams M, Li PWD, Myers EW;			
XX				
DR	WPI; 2001-656860/75.			
XX				
N-PSDB;	ABLI5900.			
XX				
PS	Disclosure; SEQ ID NO 42183; 21pp + Sequence Listing; English.			
XX				
CC	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI6176-ABLI3051), expressed DNA sequences (ABLI840-ABLI6175) and the encoded proteins (ABLI773-ABLI2072).			
CC	The sequence data for this patent did not form part of the printed			

CC receptors can be used in a novel, claimed method of screening for
 CC compounds which modulate the binding of a Wnt polypeptide (secreted
 CC proteins involved in cell-to-cell signalling) to a Wnt receptor.
 CC Wnt is involved in (mammary) cancer and other processes involving
 CC growth, development and proliferation (both normal and abnormal).
 CC Modulators identified by the claimed method are useful for
 CC treatment of diseases related to these conditions.

XX SQ Sequence 572 AA;

Query Match 33.6%; Score 440.5; DB 18; Length 572;
 Best Local Similarity 38.8%; Pred. No. 8.4e-29;
 Matches 100; Conservative 36; Mismatches 75; Indels 47; Gaps 12;

QY 8 APPSLULLALQALVGRAAAASKP-----VCQEITVPMRCRGICGNLTHMPN 53
 Db 11 SPILGCLALVLA-LIGALPTDTRAQPHGEKGISVDPDGFCQPISPCTDIAYNQTLPN 69
 QY 54 QENHTDDEAGLEVHQWPLVLEQCSPLREFCTMYPICUPDYHKLPPRSVCRAK 113
 Db 70 LIGHTNOEDAGLEVHQWPLVKVQCSPLREFCTMYPICUPDYHKLPPRSVCRAK 128

QY 114 AGCSPPLMRQYGAWPWMSCDLPVLGRDAEVLCMDYRNSEAT--TAPRPPAKPLP 170
 Db 129 QCEALANKKFGQFWPLPERLRCNPFPVHG--AGELCVGQNTSDGGAGSPTAPTYLP 186
 QY 171 GPPGAAPASGGECFPAGG-----PFVCKCREFPVILKESHLPLYNKVRNGQVNCAVPCYQ 224
 Db 187 DSPPFTAMS---PSDGRGRLSPFSCP-RQLKVP----PYLGYRFIYE-RDCGAPC-E 233

QY 225 FS-----FSADETFA 235
 Db 234 PGRLANGLMYFKEEERRFA 251

RESULT 7

ID AAB12117 standard; Protein; 647 AA.
 XX AC AAB12117;
 XX DT 02-FEB-2001 (first entry)

XX DE Hydrophobic domain protein from clone HP02539 isolated from Saos-2 cells.
 XX KW Human; secreted protein; membrane protein; hydrophobic domain;
 KW proliferation control; differentiation induction; material transport;
 KW biophyaxis; Signal receptor; ion channel; transporter; immunostimulant;
 KW immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic;
 KW haemostatic; thrombotic; anti-inflammatory; tumour inhibition; cancer;
 KW autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.
 OS Homo sapiens.

XX PN WO200029448-A2.
 XX PD 25-MAY-2000.
 XX PF 17-NOV-1999; 99WO-JP06412.
 XX PR 17-NOV-1998; 98JP-0326255.
 PR 22-DEC-1998; 98JP-0364315.
 PR 16-MAR-1999; 99JP-0069811.
 PR 27-APR-1999; 99JP-0119299.
 PR 19-MAY-1999; 99JP-0138169.

PA (SAGA) SAGAMI CHEM RES CENT.

PA (PROT-) PROTEGENE INC.
 XX PI Kato S, Kimura T;
 XX PR MPI; 2000-387753/33.
 DR N-PSDB; AAA60179, AAA60189.

XK Proteins comprising hydrophobic regions, such as secretory and membrane
 PR proteins, useful in research and diagnostics and having various
 PR activities e.g. immunomodulatory, antiinflammatory, chemokinetic,
 PR hemostatic, thrombolytic -

XX PS Claim 1; Page 178-181; 410pp; English.

XX SQ Sequence 647 AA;

Query Match 31.7%; Score 415; DB 21; Length 647;
 Best Local Similarity 36.0%; Pred. No. 1.3e-26;
 Matches 104; Conservative 30; Mismatches 87; Indels 68; Gaps 11;

QY 3 RP--DPSAPPSTLLLU-----AQLVG-RAAMASKP----- 31
 Db 43 RPPDPRRLARQLLILWLIBPLLGVRQAQQAGQQGPGQQPPPPQQQQSQQY 102
 QY 32 -----VCQEITVPMRCRGICGNLTHMPNFDHDTDEAGLEVHQWPLVSIQCS 79
 Db 103 NGERGTISVDPDHGCGQPISPCTDIAYNQTLIPNLIGHTNOEDAGLEVHQWPLVKVQCS 162

QY 80 PDLREFCTMYPICUPDYHKLPPRSVCRAKCSPLMRQYGAWPWMSCDLPV 139
 Db 163 ABKKFLGCSMVAVPCYV-LBQMLPPCRSLCBERAOCEALANKKFGQFWPLDTLKEKPVH 221

QY 140 GRDAEVICMDYRNSEAT-TAPRPPAKPLTQGGPGAPASGGECPAG-----GPVCKR 193
 Db 222 G--AGELCVGQNTSDKGKPTTSLPBFWTSNPPQHGGGGHGGGGAGSERGKFRSCP-R 278

QY 194 BPPVILKESHLPLYNKVRTGOWPNCAVPCYQPS-----FSADETFA 235
 Db 279 ALKVPSPVLYNHFLGEK-----DCGAPC-BPTKVGLMYFGPEELRFS 319

RESULT 8

ID AAB73308 standard; Protein; 581 AA.
 XX AC AAB73308;
 XX DT 22-MAY-2001 (first entry)

DE Human frizzled family protein 584.

XX Human; frizzled family gene 584; embryo; foetus; cancer;
 KW drug discovery; cytostatic.

XX Homo sapiens.

XX PN WO200112808-A1.

XX PD 22-FEB-2001.
 XX PF 18-AUG-2000; 2000WO-JP05552.

XX PR 18-AUG-1999; 99JP-0232018.

PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX
XX
PI Senoo C, Numata M;
XX WPI; 2001-211220/21.
DR N-PSDB; AAF75974.
XX
PT Novel frizzled family genes 584 strongly expressed in embryo and fetus
PT as well as in cancer cells, useful in drug development for diseases
PT with abnormal expression including tumor
XX
PS Claim 1; Fig 6-7; 89pp; Japanese.
CC The invention relates to a novel frizzled family gene, 584, from mouse
CC and human (cDNA given in AAF75973 and AAF75974), and to the mouse and
CC human 584 proteins (AAB73307, AAB73308). Gene 584 is strongly expressed
CC in the embryo and foetus, and is also strongly expressed in cancer
cells. The invention also relates to recombinant vectors and host
cells comprising gene 584 nucleic acids, the recombinant expression of
the 584 protein, methods of screening for modulators of 584 activity or
expression, and the compounds thus identified. The human and mouse 584
genes represent a novel gene target for the development of drugs useful
in the treatment of diseases such as cancer. The present sequence
CC represents human protein 584.
XX
SQ Sequence 581 AA;

```
Query Match 29.3%; Score 384; DB 22; Length 581;
Best Local Similarity 39.6%; Pred. No. 4.8e-24; Matches 82; Conservative 27; Mismatches 70; Indels 28; Gaps 7;
```

QY 1 MARIDPSAPPSSLLILLAGLUVGRALAASKRPAV-----COETIVPMERGIGNTTHPN 53
Db 1 MORPCPR-----IWLVLQMGSCAIISSMDMERPGDGKQPIBIPMCKDIGNWTRPN 54

QY 54 QFNHDTQDAGLELYHQFWLVEIQCSPDRFLCTTMYPICLPDYHKPLPPCSVCERAK 113
Db 55 LMGHBNORAAIQLHEFAPLVEYGGHGLRFFLCSLYAPNCTEQSTPIACRVMCBOAR 114

QY 114 AGCSPLMRQYGFANVERMSCDRLPVLGRDAEVLCND - VNRSEATT-----APPR 161
Db 115 LKCSPPIMEQENKFPPDSLQKLP-NKDNPPNLGMEAPNNSDEPRTGSLFPLFRQR 173

QY 162 PFPKAKPTLGQPPGAPASGBCPAGCPF 188
Db 174 PHSAQEH - PLKDGFFGRGG - CDNPCKF 198

RESULT 9
AAW11767
ID AAW11767 standard; Protein; 325 AA.
XX
AC AAW11767;
XX
DT 28-SEP-1998 (first entry).
XX
DE Human hsfz protein.
XX
KW Human; nerve cell growth factor; hsfz protein; neuronal cell
proliferation; differentiation factor.
OS Homo sapiens.
XX
DE-19702835-A1.
XX
PD 22-JAN-1998.
XX
PF 27-JAN-1997; 97DE-1002835.
XX
PR 09-JUL-1996; 96DE-1027631.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Deutsch U, Drexler JCA, Lottspeich F, Mayr T, Risau W;

PI Rohrer H;
XX
DR WPI; 1998-088096/09.
DR N-PSDB; AAV13101.
XX
PT New nucleic acid encoding protein that increases neuronal cell
PT proliferation - useful as nerve growth factor and for detection or
PT inhibition of differentiation factors
XX
PS Claim 5; Page 17; 27pp; German.
XX
CC This sequence represents the human hsfz protein. This protein is found to
increase the proliferation of neuronal cells. Such proteins can be used
as nerve cell growth factors and for the detection and/or inhibition of
differentiation factors, specifically those corresponding to the
Drosophila melanogaster wingless or mouse int-1 type.
XX
SQ Sequence 325 AA;

```
Query Match 29.0%; Score 380; DB 19; Length 325;
Best Local Similarity 36.0%; Pred. No. 5.4e-24; Matches 81; Conservative 34; Mismatches 80; Indels 30; Gaps 7;
```

QY 10 PSILLIILQAQVVERAA-----AASKAPVQCQTIVPMRCRGICQYLNLTIMPNOENHDQDEA 63
Db 6 PGGMUILLRAGLIALAALCLLRVPGARAACERVRIPACKSLPWNMTQPNHHLHSTQNA 65

QY 64 GLSVHQFWPLVIEQTCPSDLRFUCTMVTPICHY-HKPLPCCRSCERAKGCSPLMRQ 122
Db 66 IIAIEQFGSLGTHCSPDLIFLCAMAPICITDFOHEPIKECKSVGERARQGCEPILIK 125

QY 123 YGFAWPERMSCSRPLPVLGRDAVLCMDYNSRATAPPRLPFPFAKPTLPGPCGAPASGEC 182
Db 126 YRHSPWENLACHEBLPVYDGR--VCI--SPEAIVTADGAFP-----MDSSNGC 170

QY 183 PAGGPFPVKCRFPVPIKESIPL---YNKRTIQQVNPNCAPVCY 223
Db 171 RGASSERCKK---PIRATOQTYFRNNNNVIRAKVKEIKTKCH 211

RESULT 10
AAW8695
ID AAW8695 standard; Protein; 325 AA.
XX
AC AAW8695;
XX
DT 04-SEP-1998 (first entry)
XX
DE Human growth-inducing protein Frzb sequence.
XX
KW Frzb; growth-inducing protein; bovine; human; Xenopus; cartilage;
KW bone; nerve; muscle; tumour; Wnt-expressing tumour; myodegeneration;
KW subglottic stenosis; chondromalacia patellae; osteoarthritis;
KW joint surface lesion; neurodegeneration; Alzheimer's disease;
KW osteodegeneration; angiogenesis; wound healing.
OS Homo sapiens.
XX
PN WO9816641-A1.
XX
PD 23-APR-1998.
XX
PR 08-OCT-1997; 97WO-US18362.
XX
PR 20-MAR-1997; 97US-0822333.
PR 11-OCT-1996; 96US-0729452.
XX
PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Hoang B, Luyten FP, Moes M, Wang S;
XX
DR WPI; 1998-251288/22.
DR N-PSDB; AAV18254.

XX New nucleic acid encoding human, bovine and *Xenopus* Frzb protein -
 PT and related proteins, antibodies, peptide(s), vectors and
 PT transformed cells, used to induce growth of cartilage, bone, nerve,
 PT and muscle, also for inhibiting Wnt-expressing tumour
 XX PS Claim 4; Pages 37-38; 66pp; English.

CC This represents a human growth-inducing protein Frzb. Bovine, human
 CC and *Xenopus* Frzb genes which are shown in AAV18253 to AAV18255 are
 CC related to the frizzled gene in *Drosophila*. The corresponding bovine,
 CC human and *Xenopus* Frzb protein sequences are shown in AAW18694 to
 CC AAW48696. A recombinant construct containing a Frzb encoding nucleic acid
 CC linked to a heterologous promoter in an expression vector can be used to
 CC produce recombinant Frzb proteins. The Frzb proteins may be formulated
 CC with fibrin glue, freeze-dried, cartilage grafts or collagen (optionally
 CC also cartilage progenitor cells, chondroblasts or chondrocytes). They
 CC are coated on to, or mixed with, a (non-resorbable matrix, or mixed with
 CC a biodegradable polymer. They modulate activity of the growth factors
 CC Wnt 1 to 8. The Frzb proteins induce skeletal morphogenesis, embryonic
 CC pattern formation and tissue specificity and are used to induce growth
 CC of cartilage, bone, nerve and muscle, particularly in cases of
 CC subglottic stenosis, chondromalacia patellae, osteoarthritis, joint
 CC surface lesions, neurodegeneration (e.g. Alzheimer's disease), joint
 CC myodegeneration or osteodegeneration. They also modulate Wnt-mediated
 CC signalling in cells, and are used to inhibit growth of Wnt-expressing
 CC tumours (particularly mammary or intestinal). The Frzb genes may also be
 CC used to identify specific modulators or as a growth factor for cells of
 CC the chondrocyte lineage in vitro, to stimulate wound healing, to promote
 CC angiogenesis, to prevent transplant rejection and as adjunct to
 CC chemotherapy or immunotherapy. Fragments of Frzb proteins are used for
 CC detecting genetic abnormalities associated with Frzb genes.
 XX Sequence 325 AA;

Query Match 28.4%; Score 372; DB 19; Length 325;
 Best local Similarity 35.6%; Pred. No. 2.6e-23; Mismatches 80; Indels 30; Gaps 7;

Qy 10 PSULLILIAOLYGRAA-----RASKAPVCOETIVPMRGIGNTLTHMPNQFNHDDEA 63
 Db 6 PGGMILLIRAGLILALACLCILRLVRGARAAACEPRIPLKCSPLNMKPNHLHSTQANA 65
 Qy 64 GLEVHQMPFLVIEIQCSPQLRFCTMTPICPDY-HKPLPCCRSCVERAKGCSPLMRQ 122
 Db 66 IIAIEQFEGLGLGRHCSPLDLFELCAMYAPICTIDFQHEPIKCKSVCEARQGCEPILIK 125
 Qy 123 YGFAWPERMSCDRLPVLGDRDAEVLCMDYNRSEATTAPRPFPAKPTLPGPPGAPASGCC 182
 Db 126 YRHSPWENLACEBLPVYDRG--VCI--SPEAVTADGDP-----MDSSNGNC 170
 Qy 183 PAGGPFYVKCRPFVPLKESHL---YNYKRTGQVNCAPCY 223
 Db 171 RGASSERCKC---PIRATOQTYFRNNNNYVTRAKVKEIKTKCH 211

RESULT 11
 AAW41254 ID AAW41254 standard; Protein: 325 AA.
 AC AAW41254;
 XX 09-JUL-1998 (first entry)
 DE Human "frizzled" frzb-1.
 XX KW Growth factor; frizzled; frzb-1; Wnts antagonist; human;
 KW tumour suppressor; cancer.
 OS Homo sapiens.
 XX PN W09748275-A1.

RESULT 11
 AAW41254 ID AAW41254 standard; Protein: 325 AA.
 AC AAW41254;
 XX 03-AUG-1999 (first entry)
 DE Amino acid sequence of *Xenopus* clone WA129_2i.
 XX KW *Xenopus*; clone WA129_2i; embryo cDNA library; vaccine;
 KW nutrition; Cytokine; cell proliferation; cell differentiation;
 KW immune stimulating; suppression; haematoptesis; activin; inhibitor;
 KW chemotactic; chemokinetic; haemostatic; thrombolytic; cadherin;
 KW anti-inflammatory; tumour invasion suppressor; tumour inhibition.
 XX OS *Xenopus* sp.
 KW PN W0909061-A1.
 XX PD 25-FEB-1999.
 XX PF 21-AUG-1998; 98WO-US17469.

PD 24-DEC-1997.
 XX 19-JUN-1997; 97WO-US10942.
 XX 18-JUN-1997; 97US-0878474.
 PR 20-JUN-1996; 96US-0020150.
 XX PA (RGBC) UNIV CALIFORNIA.
 XX PI Bouwmeester T, De Robertis EM;
 XX DR WPI; 1998-052760/06.
 XX N-PSDB; AAV14017.
 XX New isolated growth factors - with neurotrophic, growth or
 PT differentiation factor activity, tumour growth suppressor activity
 PT or mesoderm differentiation activity
 XX PS Claim 6; FIG 9; 48pp; English.
 XX The present sequence is the human growth factor-protein
 CC "frizzled" frzb-1. frzb-1 is an antagonist of Wnts in vivo, and
 CC thus is believed to find utility as a tumour suppressor gene,
 CC since overexpressed Wnt proteins cause cancer. Frzb-1 may also be a
 CC useful vehicle for solubilisation and therapeutic delivery of
 CC complexed Wnt proteins.
 XX SQ Sequence 325 AA;

Query Match 28.4%; Score 372; DB 19; Length 325;
 Best local Similarity 35.6%; Pred. No. 2.6e-23; Mismatches 80; Indels 30; Gaps 7;

Qy 10 PSULLILIAOLYGRAA-----RASKAPVCOETIVPMRGIGNTLTHMPNQFNHDDEA 63
 Db 6 PGGMILLIRAGLILALACLCILRLVRGARAAACEPRIPLKCSPLNMKPNHLHSTQANA 65
 Qy 64 GLEVHQMPFLVIEIQCSPQLRFCTMTPICPDY-HKPLPCCRSCVERAKGCSPLMRQ 122
 Db 66 IIAIEQFEGLGLGRHCSPLDLFELCAMYAPICTIDFQHEPIKCKSVCEARQGCEPILIK 125
 Qy 123 YGFAWPERMSCDRLPVLGDRDAEVLCMDYNRSEATTAPRPFPAKPTLPGPPGAPASGCC 182
 Db 126 YRHSPWENLACEBLPVYDRG--VCI--SPEAVTADGDP-----MDSSNGNC 170
 Qy 183 PAGGPFYVKCRPFVPLKESHL---YNYKRTGQVNCAPCY 223
 Db 171 RGASSERCKC---PIRATOQTYFRNNNNYVTRAKVKEIKTKCH 211

RESULT 12
 AAY03229 ID AAY03229 standard; Protein: 325 AA.
 AC AAY03229;
 XX AAY03229;
 DT 03-AUG-1999 (first entry)
 DE Amino acid sequence of *Xenopus* clone WA129_2i.
 XX KW *Xenopus*; clone WA129_2i; embryo cDNA library; vaccine;
 KW nutrition; Cytokine; cell proliferation; cell differentiation;
 KW immune stimulating; suppression; haematoptesis; activin; inhibitor;
 KW chemotactic; chemokinetic; haemostatic; thrombolytic; cadherin;
 KW anti-inflammatory; tumour invasion suppressor; tumour inhibition.
 XX OS *Xenopus* sp.
 KW PN W0909061-A1.
 XX PD 25-FEB-1999.
 XX PF 21-AUG-1998; 98WO-US17469.

XX
PP 18-AUG-2000; 2000MO-JP05552.
XX
PR XX
18-AUG-1999; 99JP-0232018.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PT Senoo C, Numata M;
XX
DR WPI; 2001-211220/21.
XX
N-PSDB; AAF75973.

XX
PT Novel frizzled family genes 584 strongly expressed in embryo and fetus as well as in cancer cells, useful in drug development for diseases PT with abnormal expression including tumor

PS Claim 1; Fig 1; 83pp; Japanese.

XX
CC The invention relates to a novel frizzled family gene, 584, from mouse and human (cDNA given in AAF75973 and AAF5974), and to the mouse and human 584 proteins (AAB73307, AAB73308). Gene 584 is strongly expressed in the embryo and fetus, and is also strongly expressed in cancer cells. The invention also relates to recombinant vectors and host cells comprising gene 584 nucleic acids, the recombinant expression of the 584 protein, methods of screening for modulators of 584 activity or expression, and the compounds thus identified. The human and mouse 584 genes represent a novel gene target for the development of drugs useful in the treatment of diseases such as cancer. The present sequence CC represents mouse protein 584.

SQ Sequence 582 AA;

Query Match 28.3%; Score 370.5; DB 22; length 582;
Best Local Similarity 34.9%; Pred. No. 6.5e-23; Matches 87; Conservative 34; Mismatches 93; Indels 35; Gaps 10;

QY 1 MARRDDPSAPPSSLLLQLVGRAAAASKAPV-----CQEITVPMGRGIGNTIHMNP 53
Db 1 MQRPGPR-----LWVLQMQMGSCTAISWMDLERPGDGKQCPVEIPMKDIGNTRMPN 55

QY 54 QFNHDTQDEAGLETHQFLMPLVEQCSPLRFLCTMYPICLDYHKOLPPCSVVERAK 113
Db 56 LMGHENORBAIQALHEFAPLVQYGCNSHLRFELCSLYAPMCTEQSTPIACRMVCGAR 115

QY 114 AGGSPMLRQYFAMPERMSCDRLPVLGRDAEVLCMWD--YNRSEATTAAPRPFIAKPTLPG 171
Db 116 LKCSPIMQFKFWRPDSLDCSKLP-NKUDPNVLCMEAPNGSDBPSRGSGMF--PLF-- 170

QY 172 PRGAPASGBCPA--GGPVCKCREPFVPLKILSHPLNKVRGQVPRICA--VPCYQPS 226
Db 171 RPORPHSAQEHPLKGGPGRAGCDNP-----GKFHHVKESE--SCAPLCTPGVVDY 219

QY 227 FSADERTFA 235
Db 220 WSRDDDKRFA 228

SQ Sequence 589 AA;

Query Match 28.2%; Score 370; DB 22; length 589;
Best Local Similarity 40.9%; Pred. No. 7.2e-23; Matches 85; Conservative 29; Mismatches 72; Indels 22; Gaps 9;

QY 33 CQEITVPMGRGIGNTIHMNPQHDTODEALEVQYFAPMCTEQSTPIACRMVCGAR 92
Db 53 CEPITISCKNIPYNTIMPNLIGHTQBEADLVIQFAPLKIGSDDLOFLCSLYVP 112

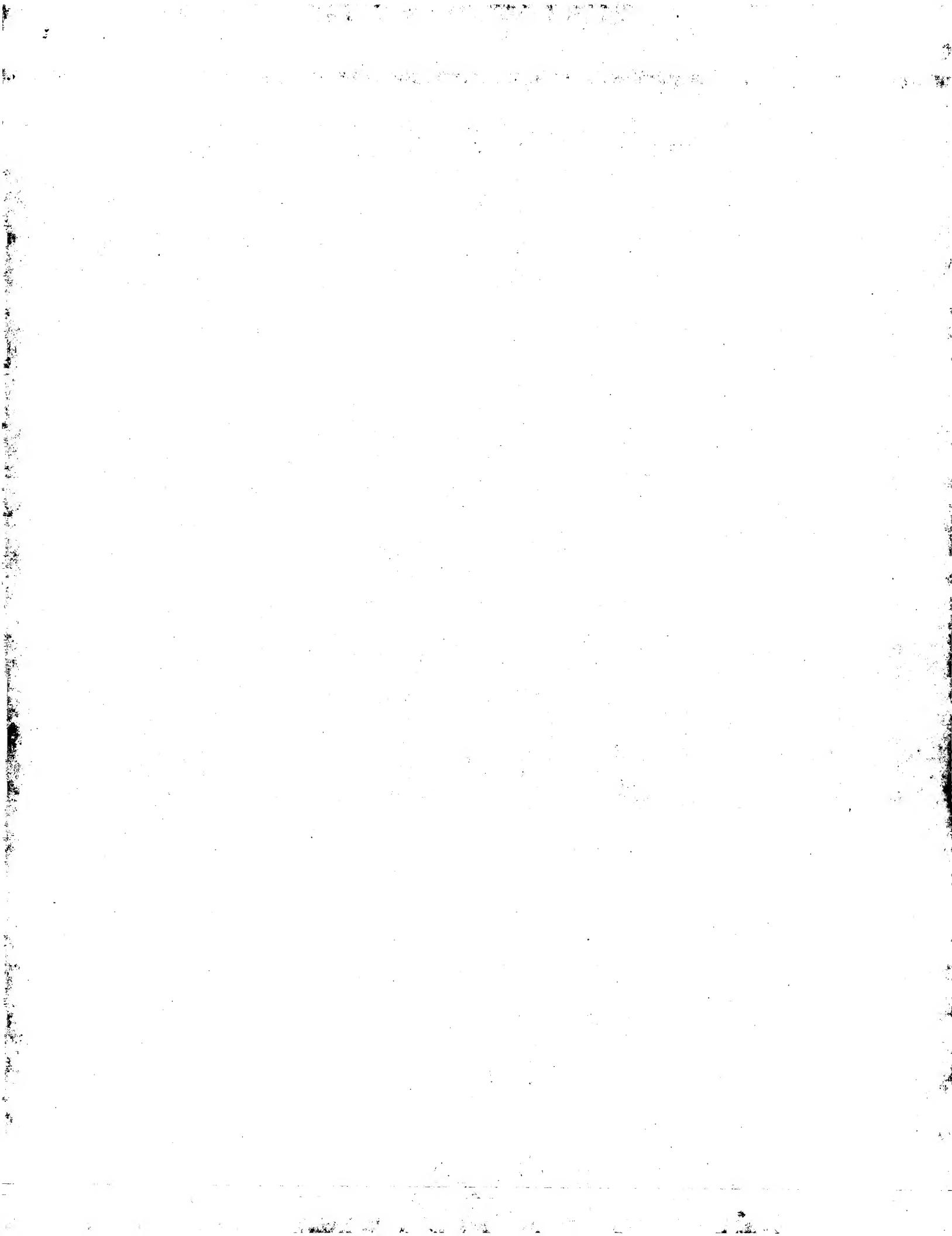
QY 93 ICIPDVKPLPCCRSVVERAKGCSPLMRQYFAMPERMSCDRLPVLGRDAEVLCMWD-- 151
Db 113 VC-TILERPIPPCRSLCESARJ-CEKUMKTTFNWNPELNLESKFPVHG--GDLCAVENT 168

QY 152 -RSEATTAAPRPFIAKPTLPGVPGAPASGBCPAGEG_PVCFCKCREPFVPI-LKESHLYN 208
Db 169 TSSASTAAATPRTSVAKT---TRKHOTGVESPHRNIGFVC-----PVQKTKPLGMY 217

QY 209 KVRTG---QVPCAVPQYQPSFADERT 233
Db 218 ELVKGKODLHQGAPCHAMFFPERERT 245

RESULT 15
ABB71245
ID ABB71245 Standard; Protein; 589 AA.
AC
XX
AC ABB71245;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 40527.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
PN WO2001/1042-A2.

Search completed: May 19, 2003, 16:34:12
Job time : 39 secs



Gencore version 5.1.4_p5_4578
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Om protein - protein search, using sw model

Run on: May 19, 2003, 16:33:37 ; Search time 15 Seconds
 (without alignments)
 460.959 Million cell updates/sec

Title: US-09-847-102A-68
 Perfect score: 1310
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 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
 Sequence 9, Application US/089337067
 Patent No. 6433155
 GENERAL INFORMATION:
 APPLICANT: Umanky, Samuel
 APPLICANT: Melkonyan, Hovsep
 TITLE OF INVENTION: A FAMILY OF GENES ENCODING
 TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
 TITLE OF INVENTION: METHODS OF USE THEREOF
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018

COMPUTER READABLE FORM:
 COMPUTER: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/08/937,067
 APPLICATION NUMBER: US/08/937,067
 FILING DATE: CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Lehnhardt, Susan K.
 REGISTRATION NUMBER: 33,943
 REFERENCE/DOCKET NUMBER: 23647-20018.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 813-5000
 TELEFAX: (650) 494-0792
 INFORMATION FOR SBO ID NO: 9,7
 SEQUENCE CHARACTERISTICS:
 LENGTH: 585 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-937-067-9

ALIGNMENTS

Query	Match	Length	DB	ID	Description
1	1310	100.0	585	4	US-08-937-067-9
2	823.5	62.9	685	4	US-08-937-067-14
3	477	36.4	565	4	US-08-937-067-8
4	440.5	33.6	572	4	US-08-937-067-13
5	372	28.4	325	4	US-08-878-474-9
6	367	28.0	323	4	US-08-878-474-7
7	360	27.5	318	4	US-08-878-474-3
8	304.5	23.2	666	4	US-08-937-067-10
9	299.5	22.9	537	4	US-08-937-067-11
10	282	21.5	706	2	US-08-987-654B-6
11	278.5	21.3	295	4	US-08-937-067-2
12	271	20.7	709	4	US-08-937-067-12
13	270	20.6	212	4	US-08-937-067-4
14	270	20.6	317	4	US-08-937-067-6
15	241.5	18.7	295	4	US-08-893-654B-7
16	234	17.9	314	2	US-08-937-067-7
17	231.5	17.7	291	4	US-08-937-067-9
18	229	17.5	280	4	US-08-893-654B-4
19	180.5	13.8	641	4	US-09-231-989-10
20	139.5	10.6	787	2	US-08-770-484A-4
21	139.5	10.6	787	4	US-08-953-823A-4
22	136	10.6	787	4	US-09-398-239-4
23	130	9.9	793	2	US-08-770-484A-2
24	130	9.9	793	4	US-08-953-823A-2
25	130	9.9	793	4	US-09-293-505-17
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3	97.5	7.4	1461	4	US-09-289-578-9
31	95.5	7.3	265	4	US-08-918-288-39
32	95.5	7.3	265	4	US-09-282-357-39
33	95	7.3	265	4	US-08-918-288-3
34	95	7.3	265	4	US-09-282-357-3
35	94.5	7.2	869	1	US-08-374-834-16
36	94.5	7.2	869	2	US-08-644-271-29
37	94.5	7.2	869	4	US-09-07-955-33
38	93.5	7.1	585	4	US-09-930-181-4
39	93.5	7.1	603	4	US-09-930-181-17
40	93.5	7.1	668	4	US-09-930-181-2
41	92	7.0	160	1	US-08-479-233-11
42	92	7.0	160	5	PCT-US93-00633-11
43	92	7.0	902	1	US-08-366-478B-6
44	92	7.0	902	1	US-08-818-823-6
45	92	6.9	868	5	PCT-US95-0843-21

Sequence 15, Appl
 Sequence 9, Appl
 Sequence 9, Appl
 Sequence 39, Appl
 Sequence 39, Appl
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 Sequence 16, Appl
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 Sequence 17, Appl
 Sequence 2, Appl
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 Sequence 6, Appl
 Sequence 6, Appl
 Sequence 21, Appl

Query	Match	Length	DB	ID	Description
1	1310	100.0	585	4	US-08-937-067-9
2	823.5	62.9	685	4	US-08-937-067-14
3	477	36.4	565	4	US-08-937-067-8
4	440.5	33.6	572	4	US-08-878-474-9
5	372	28.4	325	4	US-08-878-474-7
6	367	28.0	323	4	US-08-878-474-3
7	360	27.5	318	4	US-08-878-474-4
8	304.5	23.2	666	4	US-08-937-067-10
9	299.5	22.9	537	4	US-08-937-067-11
10	282	21.5	706	2	US-08-987-654B-6
11	278.5	21.3	295	4	US-08-937-067-2
12	271	20.7	709	4	US-08-937-067-12
13	270	20.6	212	4	US-08-937-067-4
14	270	20.6	317	4	US-08-937-067-6
15	241.5	18.7	295	4	US-08-893-654B-7
16	234	17.9	314	2	US-08-937-067-7
17	231.5	17.7	291	4	US-08-937-067-9
18	229	17.5	280	4	US-08-893-654B-4
19	180.5	13.8	641	4	US-09-231-989-10
20	139.5	10.6	787	2	US-08-770-484A-4
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22	136	10.6	787	4	US-09-398-239-4
23	130	9.9	793	2	US-08-770-484A-2
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25	130	9.9	793	4	US-09-293-505-17
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Query	Match	Length	DB	ID	Description
1	1310	9.9	803	4	US-09-293-505-15
2	97.5	7.4	1461	4	US-09-585-887-9
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31	95.5	7.3	265	4	US-08-918-288-39
32	95.5	7.3	265	4	US-09-282-357-39
33	95	7.3	265	4	US-08-918-288-3
34	95	7.3	265	4	US-09-282-357-3
35	94.5	7.2	869	1	US-08-374-834-16
36	94.5	7.2	869	2	US-08-644-271-29
37	94.5	7.2	869	4	US-09-07-955-33
38	93.5	7.1	585	4	US-09-930-181-4
39	93.5	7.1	603	4	US-09-930-181-17
40	93.5	7.1	668	4	US-09-930-181-2
41	92	7.0	160	1	US-08-479-233-11
42	92	7.0	160	5	PCT-US93-00633-11
43	92	7.0	902	1	US-08-366-478B-6
44	92	7.0	902	1	US-08-818-823-6
45	92	6.9	868	5	PCT-US95-0843-21

Query	Match	Length	DB	ID	Description
1	1310	100.0%	Score 1310:	DB 4;	Length 585;
2	97.5	100.0%	Score 97.5:	DB 4;	Length 585;
3	97.5	100.0%	Score 97.5:	DB 4;	Length 585;
31	95.5	100.0%	Score 95.5:	DB 4;	Length 585;
32	95.5	100.0%	Score 95.5:	DB 4;	Length 585;
33	95	100.0%	Score 95:	DB 4;	Length 585;
34	95	100.0%	Score 95:	DB 4;	Length 585;
35	94.5	100.0%	Score 94.5:	DB 4;	Length 585;
36	94.5	100.0%	Score 94.5:	DB 4;	Length 585;
37	94.5	100.0%	Score 94.5:	DB 4;	Length 585;
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42	92	100.0%	Score 92:	DB 4;	Length 585;
43	92	100.0%	Score 92:	DB 4;	Length 585;
44	92	100.0%	Score 92:	DB 4;	Length 585;
45	92	100.0%	Score 92:	DB 4;	Length 585;

Query	Match	Length	DB	ID	Description
1	1310	100.0%	Score 1310:	DB 4;	Length 585;
2	97.5	100.0%	Score 97.5:	DB 4;	Length 585;
3	97.5	100.0%	Score 97.5:	DB 4;	Length 585;
31	95.5	100.0%	Score 95.5:	DB 4;	Length 585;
32	95.5	100.0%	Score 95.5:	DB 4;	Length 585;
33	95	100.0%	Score 95:	DB 4;	Length 585;
34	95	100.0%	Score 95:	DB 4;	Length 585;
35	94.5	100.0%	Score 94.5:	DB 4;	Length 585;
36	94.5	100.0%	Score 94.5:	DB 4;	Length 585;
37	94.5	100.0%	Score 94.5:	DB 4;	Length 585;
38	93.5	100.0%	Score 93.5:	DB 4;	Length 585;
39	93.5	100.0%	Score 93.5:	DB 4;	Length 585;
40	93.5	100.0%	Score 93.5:	DB 4;	Length 585;
41	92	100.0%	Score 92:	DB 4;	Length 585;
42	92	100.0%	Score 92:	DB 4;	Length 585;
43	92	100.0%	Score 92:	DB 4;	Length 585;
44	92	100.0%	Score 92:	DB 4;	Length 585;
45	92	100.0%	Score 92:	DB 4;	Length 585;

Query	Match	Length	DB	ID	Description
1	1310	100.0%	Score 1310:	DB 4;	Length 585;
2	97.5	100.0%	Score 97.5:	DB 4;	Length 585;
3	97.5	100.0%	Score 97.5:	DB 4;	Length 585;
31	95.5	100.0%	Score 95.5:	DB 4;	Length 585;
32	95.5	100.0%	Score 95.5:	DB 4;	Length 585;
33	95	100.0%	Score 95:	DB 4;	Length 585;
34	95	100.0%	Score 95:	DB 4;	Length 585;
35	94.5	100.0%	Score 94.5:	DB 4;	Length 585;
36	94.5	100.0%	Score 94.5:	DB 4;	Length 585;
37	94.5	100.0%	Score 94.5:	DB 4;	Length 585;
38	93.5	100.0%	Score 93.5:	DB 4;	Length 585;
39	93.5	100.0%	Score 93.5:	DB 4;	Length 585;
40	93.5	100.0%	Score 93.5:	DB 4;	Length 585;
41	92	100.0%	Score 92:	DB 4;	Length 585;
42	92	100.0%	Score 92:	DB 4;	Length 585;
43	92	100.0%	Score 92:	DB 4;	Length 585;
44	92	100.0%	Score 92:	DB 4;	Length 585;
45	92	100.0%	Score 92:	DB 4;	Length 585;

Query	Match	Length	DB	ID	Description
1	1310	100.0%	Score 1310:	DB 4;	Length 585;
2	97.5	100.0%	Score 97.5:	DB 4;	Length 585;
3	97.5	100.0%	Score 97.5:	DB 4;	Length 585;
31	95.5	100.0%	Score 95.5:	DB 4;	Length 585;
32	95.5	100.0%	Score 95.5:	DB 4;	Length 585;
33					

RESULT 2
US-08-937-067-14
; Sequence 14, Application US/08937067
; Patent No. 6433155

GENERAL INFORMATION:
APPLICANT: Umansky, Samuel
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937, 067
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33, 943
REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-937-067-14

Query Match 62.9%; Score 823.5; DB 4; Length 685;
Best Local Similarity 60.0%; Pred. No. 2.4e-69;
Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;

QY 11 SLL-LILLALOVLGRAGAAASKAPVCOEITVPMCRGIGYNLTIMPQNDFHDDEAGLEWH 68
Db 11 SLLAALAVLQLRSQGAAGAAASKAKELACOETVPLCKGIGNYTQMPNQFNHDDEAGLEWH 70

QY 69 QFWPLVYIQCOPDLRFCLTYMTPICPDYHKLPPCRSVCERAKAGGSLMRQYGAWP 128
71 QFWPLVYIQCOPDLRFCLTYMTPICPDYHKLPPCRSVCERAKAGGSLMRQYGAWP 130

QY 129 ERMSCDRFLIPVLRDAEVLCMDYNREMTA--PPRPFPAKPTLPG-----PPG 174
131 DMRCDRCPQQ-NPDTLCMQNTDTTAASPPRLPPP----PGQPPSGSGHSRPPG 188

RESULT 3
US-08-937-067-8
; Sequence 8, Application US/08937067
; Patent No. 6433155

GENERAL INFORMATION:
APPLICANT: Umansky, Samuel
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
COUNTRY: CA
ZIP: 94304-1018

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937, 067
FILING DATE:
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33, 943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELEPHONE: (650) 813-5600

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-937-067-8

Query Match 36.4%; Score 477; DB 4; Length 565;
Best Local Similarity 41.9%; Pred. No. 6.7e-37;
Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

QY 3 RPPDPSAPPSSLUUUAQLVGRAGAAASKAPV----COEITVPMCRGIGYNLTIMPQN 55
Db 2 RPPSAPPRLPPLPPLPAGPAQFGKEKGISIDPHGFQPISTPLCTDIAYNQTMNUL 61

QY 56 NHDTODEAGLEWHQFWPLVYIQCOPDLRFCLTYMTPICPDYHKLPPCRSVCERAKAG 115
62 GHNTQEDAGLEWHQFWPLVYIQCOPDLRFCLTYMTPICPDYHKLPPCRSVCERAKAG 120

QY 116 CSPIMRQYGAWSRMSOPDLRVLGDRDEVLCDMYNRSE-----ATAPPREPA-KPT 168
121 CEALMKFGFOWBPLRRCBHFPRHG---ABQICVGQNHSDGAPALLTAPP---PGLQPG 175

QY 169 LPGPPGA-PASGGC-PAGG---PVVKCRFPVILKSHPLYNKVRTOQVNPNCAPVCKO 224
Db 176 AGGTPGGGGGAGAPPRTVATELHFKP-----RVLKV--PSLYKFLGERCAAPC-E 226

Db 227 |:| :| |:
PARPGSMFQSQERTRFA 244

RESULT 4

US-08-937-067-13

Sequence 13, Application US/08937067

Patent No. 6433155

GENERAL INFORMATION:

APPLICANT: Umansky, Samuel

TITLE OF INVENTION: A FAMILY OF GENES ENCODING

TITLE OF INVENTION: APTOTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREOF

NUMBER OF SEQUENCES: 19

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937, 067

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33, 943

REFERENCE/DOCKET NUMBER: 23647-20018. 00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 811-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 572 amino acids

TYPE: amino acid

STRANDEDNESS: Single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-937-067-13

Query Match

Best Local Similarity

Score 33.6%; Pred. No. 1.8e-33;

Length 572; DB 4;

Matches 100; Conservative

Mismatches 75; Indels 47; Gaps 12;

Query 8 APPSLILLIAQLAQVRAAAASKP-----VQEBTTVPMGIGGNLTMPN 53

Db 11 SPIGLCALVLA-LLGALLTDTRQPHGEKGTSVDPDHFCOPISIPLTDIAYNQTLPN 69

Query 54 QFNHDTDDEAGLEVPHQFWPLVETQCSPLDRFLCTMTPICPDY-HKPLPQPCRSYCECERAKGCSPLMQ 113

Db 70 LIGHTNQBDAGLEHVQFPLVKVQCSPLERFLFCMYAVPCTV-LDQAIPPCRSLCERAR 128

Query 114 AGCSPLMRQYGFWRPEMSCDRLPVLGDAEVLCMDYNRSEAT-TAPPRPPAKPLP 170

Db 129 Q3CEALMNKFGPWRPERLRCENPVHG--AGETCVGONTSDSGAGGSPTAPTYLP 186

Query 171 GFPGAPASGGECPPAGG----PFVKCKREFPVILKESHPLYNKVRGQVNCAVPCYQ 224

Db 187 DPFPTAMS---PSDGCRLLSFPSCP-RQLKPF---PVIGYRELGE-RDCGADC-E 233

RESULT 6

US-08-878-474-7

Sequence 7, Application US/08878474

Patent No. 61332

GENERAL INFORMATION:

APPLICANT: De Robertis, Edward M.

TITLE OF INVENTION: Factors

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Majestic, Parsons, Siebert & Hsue

STREET: Four Embarcadero Center, Suite 1100

CITY: San Francisco

STATE: California

COUNTRY: U.S.A.

ZIP: 94111-4106

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/878, 474

FILING DATE: 18-JUN-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/020, 150

FILING DATE: 20-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Siebert, J. Suzanne

REGISTRATION NUMBER: 28, 758

REFERENCE/DOCKET NUMBER: 3100. 002US1

TELEPHONE: 415/6248-5500

TELEFAX: 415/625418

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 325 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-08-878-474-9

Query Match

Best Local Similarity

Score 28.4%; Pred. No. 2.5e-27;

Length 325; DB 4;

Matches 80; Conservative

Mismatches 34; Indels 81; Gaps 30; Gaps 7;

Query 10 PSULLILIAQLQVGRAA-----AASKPVCOITVPMCRGIGYNLTMPNQFNHDTEA 63

Db 6 PGSMUMLURAGLILAAUCLLRVPGARAACCEPRVPLICKSPLWNNMTKMPNHLHSTQANA 65

Query 64 GHVHQFWPLVVIQCSPLDRFLCTMTPICPDY-HKPLPQPCRSYCECERAKGCSPLMQ 122

Db 66 IIAIEQEGLGLGTHCSDLLFLFCAMAPICHTDFQEPICKSYCEPARKGCCEPLIK 125

Query 123 YGFAPWERMSCRLPVLGDAEVLCMDYNRSEAT-TAPPRPPAKPLP 182

Db 126 YRHSPWENLACBLLPVYDRG---VCI---SPEAVTADGADF-----MDSSNGNC 170

Query 183 PAGGPFWVCKCRPPVPLIKESHPL---YNKVRTGQVNCAVPCYQ 223

Db 171 RGAASSERCKCK---PIRATQTYFRNNNTYVIRAKVEIKEIKCH 211

RESULT 5

NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Majestic, Parsons, Siebert & Haue
 STREET: Four Embarcadero Center, Suite 1100
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 94111-4106

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/878,474
 FILING DATE: 18-JUN-1997
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/020,150
 FILING DATE: 20-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Siebert, J. Suzanne
 REGISTRATION NUMBER: 28,758
 REFERENCE/DOCKET NUMBER: 3100.002US1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/248-5500
 TELEFAX: 415/362-5418
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 323 amino acids
 TYPE: amino acid
 MOLECULE TYPE: Peptide
 ; US-08-878-474-7

Query Match 28.0%; Score 367; DB 4; Length 323;
 Best Local Similarity 35.8%; Pred. No. 7.3e-27;
 Matches 77; Conservative 34; Mismatches 80; Indels 24; Gaps 6;

Qy 14 LILILALQLVGRAAASKAPVCQEBITPMCGIGIGYNTLHMNPQFNHDQDAGLEVHOFWPL 73
 Db 16 LIVLVACLCLIQVPGQAACECPVRPLCKSLPWNMVKMPHLHSTQANAILAMQFGL 75

Qy 74 VEIQSPDRFLCTMYTICLDPY-HKPLPPCRSCVERAKAGGSPLMROYGAPEWMS 132
 Db 76 LGTHCSDPLFLFCAMYAPCTIDQHEPKTICKSVCERAROGCPIKLKYRHSWPESLIA 135

Qy 133 CDRDVVLGRDAEVLQMDYNSEATTAPPRDFPAKTLPGPGAPASGGCAGGCFVCKC 192
 Db 136 CDELVLYDVRG--VCI--SBEAIVADGADFP----MDSSSTGHRCGASSSERCKC 180

Qy 193 REPVFPILKSHPL---YNYVRTQVNPNCAPCY 223
 Db 181 K---PVRA-TQKTHFRNNYKVIRAKVKEVKVKCH 211

RESULT 7
 US-08-878-474-3
 ; Sequence 3, Application US/08878474
 ; Patent No. 6133232
 ; GENERAL INFORMATION:
 ; APPLICANT: De Robertis, Edward M.
 ; APPLICANT: Bouwmeester, Tewis
 ; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: Majestic, Parsons, Siebert & Haue
 ; STREET: Four Embarcadero Center, Suite 1100
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 94111-4106

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/878,474
 FILING DATE: 18-JUN-1997
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/020,150
 FILING DATE: 20-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Siebert, J. Suzanne
 REGISTRATION NUMBER: 28,758
 REFERENCE/DOCKET NUMBER: 3100.002US1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/248-5500
 TELEFAX: 415/362-5418
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 318 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-878-474-3

Query Match 27.5%; Score 360; DB 4; Length 318;
 Best Local Similarity 37.1%; Pred. No. 3.2e-26;
 Matches 83; Conservative 34; Mismatches 73; Indels 34; Gaps 10;

Qy 8 APPSLILLALQLVGRAAASKAPVCQEBITPMCGIGIGYNTLHMNPQFNHDQDAGLEV 67
 Db 14 AIPGLALLIP---NAYCAS---CEPVIRPMCKSMWNMTKPNFHLSHTOANAILAI 65

Qy 68 HQFMPVLVEIQSPDRFLCTMYTICLDPY-HKPLPPCRSCVERAKAGGSPLMROYGAPEWMS 132
 Db 66 EQFGLLTTESQDLFLFCAMYAPCTIDQHEPKTICKSVCERAROGCPIKLKYRHSWPESLIA 125

Qy 127 WPERMSCDPLVIGRDAEVICIMYNSRATTAAPPRPFPAKTLPGPGAPASGGCAGGCFVCKC 186
 Db 126 WPESIACELLPVYRG--VCIS--PERAVTVEQGTDSPDF---SMDSNNGCNSGR 175

Qy 187 PFVCKCREFPVPI----LKESHPLYNKVRGQVNPNCAPCY 223
 Db 176 EH-CKCK----PMKATOKTYLKN--YNYVIRAKVKEVKVKCH 211

RESULT 8
 US-08-937-067-10
 ; Sequence 10, Application US/08937067
 ; Patent No. 6433155
 ; GENERAL INFORMATION:
 ; APPLICANT: Umnansky, Samuel
 ; APPLICANT: Melkonyan, Hovsep
 ; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
 ; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: MORRISON & FOOSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1018

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,067

FILING DATE: ;
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Lehnhardt, Susan K.
 REGISTRATION NUMBER: 33,943
 REFERENCE/DOCKET NUMBER: 23647-20018.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 813-5600
 TELEFAX: (650) 494-0792
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 537 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-937-067-10

Query Match 23.2%; Score 304.5; DB 4; Length 666;
 Best Local Similarity 34.5%; Pred. No. 1; 3e-20; Mismatches 27; Indels 49; Gaps 10;
 Matches 80; Conservative

QY 12 LULLLAQOLVGRAAAASKAPVCOETTPMCRGIGYNLTHMPNOFNHDQDEAGLEHQFW 71
 Db 12 LULLLAQOLVGRAAAASKAPVCOETTPMCRGIGYNLTHMPNOFNHDQDEAGLEHQFW 66

QY 72 PLVEIQQSPPDLRPLFLCTMTPICLPPDVKPLPCCRSCYERAKAGCSPLMRQYGAPEW 131
 Db 67 PMVNLDCSRDFPFLCALIYAPIOW-EYGRVTLPCLRLQRAYNSECSEKLMEMFGVPMWEDM 125

QY 132 SCDRLPVLGDRDAEVLCDMDYNRSEATTAPRPFPAKPTLPGPP--GAPAS---GGCPCA 184
 Db 126 ECSRFP---DCD-----EPYPRVLNDLNGDPTEGAPVAVORDYGFNCP- 166

QY 185 GGPFPVCKCREPFVPIKESHPL-YNKRTGQVNCAYCQPSFSADERTFA 235
 Db 167 -----RE-----LKIDPDGYSLF--HVRCSCPNNMFRRELSFA 202

RESULT 9
 US-08-937-067-11
 ; Sequence 11, Application US/08937067
 ; Patent No. 6431155
 GENERAL INFORMATION:
 APPLICANT: Umaneky, Samuil
 APPLICANT: Melkonyan, Hovsep
 TITLE OF INVENTION: A FAMILY OF GENES ENCODING
 TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
 TITLE OF INVENTION: METHODS OF USE THEREOF
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 FILING DATE: 09-DEC-1997
 APPLICATION NUMBER: US/08/987, 289
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/048, 725
 FILING DATE: 02-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: PRISTIA, PAUL F
 REGISTRATION NUMBER: 23, 031
 REFERENCE/DOCKET NUMBER: GH/70060
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 706 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-987-209-2

Query Match 22.9%; Score 299.5; DB 4; Length 537;
 Best Local Similarity 34.1%; Pred. No. 3e-20; Mismatches 32; Indels 15; Gaps 4;
 Matches 59; Conservative

QY 14 LULLLAQOLVGRAAAASKAPVCOETTPMCRGIGYNLTHMPNOFNHDQDEAGLEHQFW 73
 Db 28 LULLRPTRIGFGBEER--COPIRIANQNQGYNVTKPNLUGHEQTDALQLTRPTPL 85

QY 74 VLIQCSPLDRFLCTMTPICLPPDVKPLPCCRSCYERAKAGCSPLMRQYGAPEW 133
 Db 86 IOKGCSSQLOFFLCSVTPMCRKINIPGPGGMCLSVKRCECPVNLREFGRGAWPDTLNC 145

QY 134 DRFLPVLGDRDAEVLCDMDYNRSEATTAPRPFPAKPTLPGPPGAPASGECPAGG 186
 Db 146 SFRPP-QNDHNINCMBGPGBSVPVPLHKT-PIT-----GEBCHAVG 185

RESULT 10
 US-08-987-209-2
 ; Sequence 2, Application US/08987289
 ; Patent No. 599098
 GENERAL INFORMATION:
 APPLICANT: HU, ERDING
 APPLICANT: ZHU, YUAN
 TITLE OF INVENTION: A Human 7-TM Receptor Similar
 TITLE OF INVENTION: to Murine Frizzled-6 gene
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RATHNER & PRESTIA
 STREET: P. O. Box 980
 CITY: VALLEY FORGE
 STATE: PA
 COUNTRY: USA
 ZIP: 19482

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 FILING DATE: 09-DEC-1997
 APPLICATION NUMBER: US/08/987, 289
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/048, 725
 FILING DATE: 02-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: PRISTIA, PAUL F
 REGISTRATION NUMBER: 23, 031
 REFERENCE/DOCKET NUMBER: GH/70060
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 706 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-987-209-2

Query Match 21.5%; Score 282; DB 2; Length 706;

Best local Similarity 30.8%; Pred. No. 1.8e-18; Mismatches 80; Indels 44; Gaps 6; Matches 65; Conservative 22; Mismatches 80; Indels 44; Gaps 6; Score 278.5; DB 4; Length 295; Best Local Similarity 36.2%; Pred. No. 1.3e-18; Mismatches 63; Conservative 27; Mismatches 61; Indels 23; Gaps 7; Query Match 6 PSAPPSSLLQIQLAQ-----LVEAAASAKAPVQEI-TVPQMRGIGNLNTHMPNQHNDTQDAGLEVHQ 69 Db 2 PROPSASLLVLVASHCCLGSSARGFLFGPDFSYKRTCKPPIANOLCHGIEYQNNRIP 61 QY 53 NQENHDTDEAGLEWHQFW-PLVEIQCSPDLREFLTWTPICUPDYIKPLPCRSYCR 111 Db 62 NLIGHTETMKEV-LBQAGAWIPLVMRKQCHBDTKEFLCSLFAVCLDDDTIQPCHSLCVQ 120

RESULT 11
US-08-937-067-2
; Sequence 2, Application US/08937067
; Patent No. 6433155

GENERAL INFORMATION:
APPLICANT: Umanky, Samuil
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patient In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: 1994-03-10
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-937-067-12
Query Match 10 PSULLLIAQYGRAAASKAPVQEI-TVPQMRGIGNLNTHMPNQHNDTQDAGLEVHQ 69
Best Local Similarity 30.6%; Pred. No. 2e-17; Mismatches 71; Conservative 22; Mismatches 95; Indels 44; Gaps 8; Matches 61; Score 271; DB 4; Length 709;

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-937-067-2
Query Match 112 AKAGCSPSLMRQGFPAWPERMSDRFLPVLRDAEVLCMDYNRE---ATTAPPR 161
Best Local Similarity 36.2%; Pred. No. 1.3e-18; Mismatches 63; Conservative 27; Mismatches 61; Indels 23; Gaps 7; Score 278.5; DB 4; Length 295; Matches 65; Conservative 22; Mismatches 80; Indels 44; Gaps 6; Score 278.5; DB 4; Length 295; Best Local Similarity 36.2%; Pred. No. 1.3e-18; Mismatches 63; Conservative 27; Mismatches 61; Indels 23; Gaps 7; Query Match 121 VVKRCAPVMSAFGFPWPFDMLEDRFP---QDND-LCIPASSDHLLPATEEPAK 170
Db 121 VVKRCAPVMSAFGFPWPFDMLEDRFP---QDND-LCIPASSDHLLPATEEPAK 170
QY 130 RMSCDRFLPVLGDAEVLCMDYNRESEATTAPPRPAKPTLCPGPGAPASCGCPCAGGPV 189
Db 120 EIBCNRLP-----HCDD-----TVPVSHP-HTELSGP---QRKSDQVRDGFW 160
QY 130 RMSCDRFLPVLGDAEVLCMDYNRESEATTAPPRPAKPTLCPGPGAPASCGCPCAGGPV 189
Db 120 EIBCNRLP-----HCDD-----TVPVSHP-HTELSGP---QRKSDQVRDGFW 160
QY 190 CKCREPFPVILKESHPLYNKRTGQ-----VPNCAPVCPYQFSADERTA 235
Db 161 C-----PKHLRISGDQGYRFIGEQCAPPCPWNMFKSDELFA 198
QY 190 CKCREPFPVILKESHPLYNKRTGQ-----VPNCAPVCPYQFSADERTA 235
Db 161 C-----PKHLRISGDQGYRFIGEQCAPPCPWNMFKSDELFA 198

RESULT 13
US-08-937-067-4
; Sequence 4, Application US/08937067

Patent No. 6431155
 GENERAL INFORMATION:
 APPLICANT: Umansky, Samuel
 TITLE OF INVENTION: A FAMILY OF GENES ENCODING METHODS OF USE THEREBY AND NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,067
 FILING DATE:
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Leinhardt, Susan K.
 REGISTRATION NUMBER: 33,943
 REFERENCE DOCKET NUMBER: 23647-20018.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 813-5600
 TELEFAX: (650) 494-0792
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 212 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-937-067-4
 Query Match 20.6%; Score 270; DB 4; Length 212;
 Best Local Similarity 31.3%; Pred. No. 5.6e-18; Mismatches 81; Indels 52; Gaps 10;
 Matches 73; Conservative
 ;
 Qy 9 PSPLILLLAQ-----LVRGAAASKAPVQBI-TVPMCRGIGYNLTHMPNQF 55
 Db 5 PGSILLFLFLASHCCLGSGARGLFLFGQDPSYKRSNCBIPANLQLCHGIEYQNMRLNL 64
 Qy 56 NHDTQDEAGLEHQFW PLVEIQCSPDLRFLCTMYPICLDYHKLPUPCCSVCEAKA 114
 Db 65 GRBTMKEV-LEQAGAWPLVMKQCHPDKKKFLCSLFAPVCLDDETIOPCHSXCVQWD 123
 Qy 115 GSPLMRQYGFAPWERMSCDRPLVGRDAEVLCMDVNSEATTPRRPFPAKPTLGPG 174
 Db 124 RCPVMSAFGGFPWMPMCDRPE--QDND-LCIPASSD-----HLLPATEE 167
 Qy 175 APASGECGPAGGPFVCK-----CRPPVPLIKESHPLNKVKTGQ 214
 Db 168 APK--VCEA----CKNKNDDNDIMETLCKNDALKIVKVEITYNRRGR 212
 RESULT 14
 US-08-937-067-6
 Sequence 6, Application US/08937067
 Patient No. 6431155
 GENERAL INFORMATION:
 APPLICANT: Umansky, Samuel
 TITLE OF INVENTION: A FAMILY OF GENES ENCODING METHODS OF USE THEREBY AND NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 ADDRESS: MORRISON & FOERSTER
 ATTORNEY/AGENT INFORMATION:
 NAME: MEINERT, M.C.

STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,067
 FILING DATE:
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Leinhardt, Susan K.
 REGISTRATION NUMBER: 33,943
 REFERENCE DOCKET NUMBER: 23647-20018.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 813-5600
 TELEFAX: (650) 494-0792
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 317 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-937-067-6
 Query Match 20.6%; Score 270; DB 4; Length 317;
 Best Local Similarity 38.2%; Pred. No. 9.2e-18; Mismatches 50; Indels 10; Gaps 5;
 Matches 52; Conservative
 ;
 Qy 28 SRAVQVBI-TVPMCRGIGYNLTHMPNQFHDTCDEAGLEHVPHQPLVPCSPOLRF 85
 Db 48 SKPQCDIDPAPDPLCPTVGKRMPLNLHESLAEVKQDASSWPLAKRKHSQTQVF 107
 Qy 86 LCTMYTPICTDPYHKLPUPCCSVCEAKAGGSPLMRQYGRAWPERMSCDRLPVLGRDAEV 145
 Db 108 IGSLEARVCL---DRIVPCSLCEAVRAGCPLMEAYGFPEWPMUHCKEP-LDND--- 160
 Qy 146 LCMVNRE-ATTAPP 160
 Db 161 IGTIAVQFGHLPTAPP 176
 RESULT 15
 US-08-893-654B-6
 Sequence 6, Application US/08893654B
 Patent No. 616548
 GENERAL INFORMATION:
 APPLICANT: RACIE, LISA, ET ALIA
 TITLE OF INVENTION: Frazzled NUCLEOTIDE SEQUENCES, COMPOSITIONS AND USES
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENETICS INSTITUTE, INC.
 STREET: 87 CAMBRIDGE PARK DRIVE
 CITY: CAMBRIDGE
 STATE: MA
 COUNTRY: USA
 ZIP: 02140-2297
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/893,654B
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MEINERT, M.C.

REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5279
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8574
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-893-654B-6

Query Match 18.7%; Score 244.5; DB 4; Length 295;
Best Local Similarity 39.3%; Preq. No. 2.1e-15; Matches 42; Conservatve 22; Mismatches 38; Indels 5; Gaps 2;
QY 33 CQEIT--TVMCRGIGYNLTHMPNOFNHDITQDEAGLEVHQFWPLVETQCSPLDRFFLCMY 90
Db 38 CMRIPKSMALCYDGYSERIPNLHEMAEQQSSSWLPLARECHPDARIFLCSLP 97
QY 91 TPICLIPDWYKPLPPRSYCEAKAGCSPIMRQGFAWIERSMSCDRLP 137
Db 98 APICCFDRY---IPPCRSICEAVRSSCAPIMACGYPPWPIILKCDKFP 141

Search completed: May 19, 2003, 16:35:59
Job time : 18 secs

Db 181 ECPAGGPVCKCREPFVPIKESHPPLYNKURTGQVNCAPVPCYQPSFSADERTFA 235

Sequence 51, Application US/09847102A
 Publication No. US2003044409A1
 GENERAL INFORMATION:
 APPLICANT: University of California
 APPLICANT: Carson, Dennis A.
 APPLICANT: Rhee, Chae-Seo
 APPLICANT: Lorenzo, Leoni M.
 APPLICANT: Malini, Sen

RESULT 2
 US-10-146-474-9
 Sequence 9, Application US/10146474
 Publication No. US2003023061A1
 GENERAL INFORMATION:
 APPLICANT: Umansky, Samuel
 TITLE OF INVENTION: A FAMILY OF GENES ENCODING APOTOTIC-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
 SOFTWARE: Patentin Release #1.0, Version #1.30

APPLICATION NUMBER: US/10/146,474

FILING DATE: 14-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,067

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
 LENGTH: 585 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-146-474-9
 Query Match 100.0%; Score 1310; DB 9; Length 585;
 Best Local Similarity 100.0%; Pred. No. 2.7e-97;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARPDPSAPPSSLLLLAQOLVGRAAAASKAPVCOETIVPMCRGIGNLTHMPNQFNHDHQ 60

Db 1 MARPDPSAPPSSLLLLAQOLVGRAAAASKAPVCOETIVPMCRGIGNLTHMPNQFNHDHQ 60

Qy 61 DRAGLEYHQFLPVLVELQCSPIRREFLCTMYTCIPLYKPLUPRSVCERAKAGCSPLM 120

Db 61 DRAGLEYHQFLPVLVELQCSPIRREFLCTMYTCIPLYKPLUPRSVCERAKAGCSPLM 120

Qy 121 RQYGFAMPERMSCDRLPVLGDRREVLMCDYRNSEATTAPPRPPAKPTLQCPGPGAPASGG 180

Db 121 RQYGFAMPERMSCDRLPVLGDRREVLMCDYRNSEATTAPPRPPAKPTLQCPGPGAPASGG 180

Qy 181 ECPAGGPVCKCREPFVPIKESHPPLYNKURTGQVNCAPVPCYQPSFSADERTFA 235

Db 181 ECPAGGPVCKCREPFVPIKESHPPLYNKURTGQVNCAPVPCYQPSFSADERTFA 235

RESULT 4
 US-10-152-548-10
 Sequence 10, Application US/10152548
 Publication No. US2003044005A1
 GENERAL INFORMATION:
 APPLICANT: Bhambhani, Purunita
 Brink, Marcel
 Harryman, Cindy S.
 Wang, Yanshu
 Hsieh, Jen-chih
 Andrew, Deborah
 Nathans, Jeremy
 Nuse, Roel
 Title of Invention: Wnt Receptor Compositions and Methods
 Number of Sequences: 18
 Correspondence Address:
 Address: Dehlinger & Associates
 Street: 350 Cambridge Avenue, Suite 250
 City: Palo Alto
 State: CA
 Country: USA
 Zip: 94306
 Computer Readable Form:
 Medium Type: Floppy disk
 Computer: IBM C compatible
 Operating System: PC-DOS/MS-DOS
 Software: Patentin Release #1.0, version #1.25
 Current Application Data:
 Application Number: US/10/152,548
 Filing Date: 21-May-2002

RESULT 3
 US-09-847-102A-51

PRIOR CLASSIFICATION: <Unknown>
 APPLICATION DATA:
 FILING DATE: 11-APR-1997
 APPLICATION NUMBER: US 60/015,307
 FILING DATE: 12-APR-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Shultz, Charles K.
 REGISTRATION NUMBER: 38,615
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0980
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 586 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYDROPHOBICITY: NO
 ANTI-SENSE: NO

ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Hfz5 protein
 US-10-152-58-10

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 Query Match 100.0%; Score 1310; DB 9; Length 586;
 Best Local Similarity 100.0%; Pred. No. 2.7e-97;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MARPDAPSAPPSSLLILQLAQVGRAAAASKAVQCEITVPMCRGIGLYNLTHMPNQFNHDQ 60
 Db 1 MARPDAPSAPPSSLLILQLAQVGRAAAASKAVQCEITVPMCRGIGLYNLTHMPNQFNHDQ 60
 Qy 61 DEAGLEHOFWPLVETQCSPPDRFLCTMTCYPTICLDPYHKPLPPCRSYCERAKAGCSPLM 120
 Db 61 DEAGLEHOFWPLVETQCSPPDRFLCTMTCYPTICLDPYHKPLPPCRSYCERAKAGCSPLM 120
 Qy 121 ROYGFAMPERMSCDRLPVLGDAEVLCMDYNSEATTAPEPPPAKPTLPGPAGPASGG 180
 Db 121 ROYGFAMPERMSCDRLPVLGDAEVLCMDYNSEATTAPEPPPAKPTLPGPAGPASGG 180
 Qy 181 ECPAGGPFFVKCREPPVPILKESHPLYNKVQTGQVNCAVPCYQPSFSADERTFA 235
 Db 181 ECPAGGPFFVKCREPPVPILKESHPLYNKVQTGQVNCAVPCYQPSFSADERTFA 235
 RESULT 5
 US-09-847-102A-38
 ; Sequence 38, Application US/09847-102A
 ; Publication No. US20030044409A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of California
 ; APPLICANT: Carson, Dennis A.
 ; APPLICANT: Rhee, Chae-Seo
 ; APPLICANT: Lorenzo, Leoni M.
 ; APPLICANT: Malini, Sen
 ; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
 ; STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
 ; FILE REFERENCE: 22000-20629.00
 ; CURRENT APPLICATION NUMBER: US/09/847,102A
 ; CURRENT FILING DATE: 2001-05-01
 ; NUMBER OF SEQ ID NOS: 138
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 73
 ; LENGTH: 277
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-847-102A-73

Best Local Similarity 87.2%; Pred. No. 2.1e-81; Mismatches 0; Indels 30; Gaps 1;
 Matches 205; Conservative 0; Mismatches 0; Indels 30; Gaps 1;
 Qy 1 MARPDAPSAPPSSLLILQLAQVGRAAAASKAVQCEITVPMCRGIGLYNLTHMPNQFNHDQ 60
 Db 1 MARPDAPSAPPSSLLILQLAQVGRAAAASKAVQCEITVPMCRGIGLYNLTHMPNQFNHDQ 60
 Qy 61 DEAGLEHOFWPLVETQCSPPDRFLCTMTCYPTICLDPYHKPLPPCRSYCERAKAGCSPLM 120
 Db 61 DEAGLEHOFWPLVETQCSPPDRFLCTMTCYPTICLDPYHKPLPPCRSYCERAKAGCSPLM 120
 Qy 121 ROYGFAMPERMSCDRLPVLGDAEVLCMDYNSEATTAPEPPPAKPTLPGPAGPASGG 180
 Db 121 ROYGFAMPERMSCDRLPVLGDAEVLCMDYNSEATTAPEPPPAKPTLPGPAGPASGG 180
 Qy 181 ECPAGGPFFVKCREPPVPILKESHPLYNKVQTGQVNCAVPCYQPSFSADERTFA 235
 Db 181 ECPAGGPFFVKCREPPVPILKESHPLYNKVQTGQVNCAVPCYQPSFSADERTFA 235
 RESULT 6
 US-09-847-102A-73
 ; Sequence 73, Application US/09847102A
 ; Publication No. US20030044409A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of California
 ; APPLICANT: Carson, Dennis A.
 ; APPLICANT: Rhee, Chae-Seo
 ; APPLICANT: Lorenzo, Leoni M.
 ; APPLICANT: Malini, Sen
 ; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
 ; STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
 ; FILE REFERENCE: 22000-20629.00
 ; CURRENT APPLICATION NUMBER: US/09/847,102A
 ; CURRENT FILING DATE: 2001-05-01
 ; NUMBER OF SEQ ID NOS: 138
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 73
 ; LENGTH: 277
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-847-102A-73

Query Match 62.9%; Score 824; DB 9; Length 277;
 Best Local Similarity 59.9%; Pred. No. 1.1e-58;
 Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;
 Qy 11 SLL---ILLADQVGRAAAASKAVQCEITVPMCRGIGLYNLTHMPNQFNHDQDEAGLEVH 68
 Db 11 SLLAALLLORRSGAAASKAELACOBITVPLCKGIGNYNTYMPNQFNHDQDEAGLEVH 70
 Qy 69 QFWPLVETQCSPPDRFLCTMTCYPTICLDPYHKPLPPCRSYCERAKAGCSPLMQIGFAWP 128
 Db 71 QFWPLVETQCSPPDRFLCTMTCYPTICLDPYHKPLPPCRSYCERAKAGCSPLMQIGFAWP 130
 Qy 129 ERMSCORLPVLGDAEVLCMDYNSRBTAA--PPRPPAKPTLPG-----PPG 174
 Db 131 DMRCDRLPEOG-NPDTLCMDYNTDLTTAAPSPPRLPPP--PGEQPGSGHGRPPG 187
 Qy 175 A-----PASGG-----ECPAGGPFF---CXPAGGPFF---CXCREPPVPILESHP 205
 Db 188 APPRHGGGGGGDAAPPRGGGGKARPPGGGAARCPCEPGCOPRAMPVSSEERHP 247
 ; CURRENT FILING DATE: 2001-05-01
 ; NUMBER OF SEQ ID NOS: 138
 ; SOFTWARE: FabSeq for Windows Version 4.0
 ; SEQ ID NO: 38
 ; LENGTH: 516
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-847-102A-38
 ; Sequence 38, Application US/09847-102A
 ; Publication No. US20030044409A1
 RESULT 7
 US-09-847-102A-56
 ; Sequence 56, Application US/09847102A
 ; Publication No. US20030044409A1

GENERAL INFORMATION:
 APPLICANT: University of California
 APPLICANT: Carson, Dennis A.
 APPLICANT: Corr, Maripat
 APPLICANT: Rhee, Chae-Seo
 APPLICANT: Lorenzo, Leoni M.
 APPLICANT: Malini, Sen
 TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
 FILE REFERENCE: 22000-2029.00
 CURRENT APPLICATION NUMBER: US/09/847,102A
 CURRENT FILING DATE: 2001-05-01
 NUMBER OF SEQ ID NOS: 138
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 56
 LENGTH: 694
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-847-102a-56

Query Match 62.9%; Score 824; DB 9; Length 694;
 Best Local Similarity 59.9%; Pred. No. 2.8E-58; Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;

Qy 11 SLL--LILLAQDUGVGRAAAASKAPVCOBIVTPMRCGIGNLTHMPNGPNHDIDOEAGLEHV 68
 Db 11 SLLAAALAVIQLQRSSGAAASAKBLACOBIIVPLCKIGGYNTYMPNGPNHDIDOEAGLEHV 70

Qy 69 QFWPLVETQCSIDLRLFLCTMTPICPDYKPLPORSVERAKAGCSPLMRQGFAMP 128
 Db 71 QFWPLVETQCSIDLKFLCSMYTPICLDYKPLPCCRSVCERAKAGCPLMRQGFAMP 130

Qy 129 ERNSCDRLPVLRGLDAEVLCMDYNRSEATA--PPRPFPAKPTLPG-----PPG 174
 Db 131 DRMRCDLPEQG-NPDTLCMDYNRDLTTAAPSPPRLLPPP-PGEQPSSGHRSPPG 188

Qy 71 QFWPLVETQCSIDLKFLCSMYTPICLDYKPLPCCRSVCERAKAGCPLMRQGFAMP 130
 Db 129 ERNSCDRLPVLRGLDAEVLCMDYNRSEATA--PPRPFPAKPTLPG-----PPG 174

Qy 131 DRMRCDLPEQG-NPDTLCMDYNRDLTTAAPSPPRLLPPP-PGEQPSSGHRSPPG 188

Qy 69 QFWPLVETQCSIDLRLFLCTMTPICPDYKPLPORSVERAKAGCSPLMRQGFAMP 128
 Db 71 QFWPLVETQCSIDLKFLCSMYTPICLDYKPLPCCRSVCERAKAGCPLMRQGFAMP 130

Qy 175 A-----PASGG-----ECPPGPFV---CKCREPFVILKSHP 205
 Db 188 ARPPHRGGGGGGGDAAPPARGGGGGKARPPGGAAPCEPGCQCRAPMVSVSERHP 247

Qy 206 LYKVRWTCQVPNCACPVQPSFISADERTF 234
 Db 248 LYRVKVTKQIANCALPCHNPFPSQDERAF 276

RESULT 8
 US-09-847-102a-74
 Publication No. US2003004409A1
 Sequence 74, Application US/09/47102A

GENERAL INFORMATION:
 APPLICANT: University of California
 APPLICANT: Carson, Dennis A.
 APPLICANT: Corr, Maripat
 APPLICANT: Rhee, Chae-Seo
 APPLICANT: Lorenzo, Leoni M.
 APPLICANT: Malini, Sen
 TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 ZIP: 94306

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/152,548
 FILING DATE: 21-May-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/832,340
 FILING DATE: 11-ABR-1997
 APPLICATION NUMBER: US 60/015,307
 FILING DATE: 12-ABR-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 REFERENCE/DOCKET NUMBER: 8600-0167.30

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0960
 TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NOS: 16

SEQUENCE CHARACTERISTICS:
 LENGTH: 682 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

Query Match 62.9%; Score 823.5; DB 9; Length 274;
 Best Local Similarity 60.0%; Pred. No. 1.1e-58;
 Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;
 SEQ ID NO 74
 LENGTH: 274
 TYPE: PRT
 ORGANISM: Mouse
 US-09-847-102a-74

ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Mf28 protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16;
US-10-152-548-16

Query Match 62.9%; Score 823.5; DB 9; Length 682;
Best Local Similarity 60.0%; Pred. No. 3e-58; Mismatches 39; Indels 43; Gaps 8;
Matches 159; Conservative 24; MisMatches 39; Indels 43; Gaps 8;

Query Match 62.9%; Score 823.5; DB 9; Length 685;
Best Local Similarity 60.0%; Pred. No. 3e-58; Mismatches 39; Indels 43; Gaps 8;
Matches 159; Conservative 24; MisMatches 39; Indels 43; Gaps 8;

Qy 11 SLL-LLLAQVGRAAAASKAPKVCQETTVPMRGIGNLTHMPNQFNHDTOEAGLEVH 68
Db 11 SLLAALAVLQRSSGAAASAKELACOBITVPLCKGIGNYTIPMPNQFNHDTOEAGLEVH 70

Qy 69 QWPMLVEIQCSPLRFLFLCTMYPICLDPYKHLPLPPCRSVERAKAGCSPLMRQGFAMP 128
Db 71 QWPMLVEIQCSPLDKFLCLSMYTPICLDPYKHLPLPPCRSVERAKAGCSPLMRQGFAMP 130

Qy 129 ERMSCDLPVLGRDAEVLCMDYRNRSBATA--PPRPPAKTLPG-----PPG 174
Db 131 DRMRCDLPLEQG-NPDTLCMDYRNRTDUTAAPSPRRRLPPPP-PGEQPPSGHSRPPG 188

Qy 175 A-----PASGGEC--PAGGPFY---CKCREPPVPLIKESHPLYNK 209
Db 189 APPHRGGSSRGDDAAAPPSRGKKARPPIGGAAACCEPGCOCRAPMVSVSSERHPLYNR 248

Qy 210 VRTGQVNCAVPCYQPSFSADERTF 234
Db 249 VKTGQIANCALPCNPPFSQDERAF 273

RESULT 10
US-10-146-474-14
Sequence 14, Application US/10146474
Publication No. US20030023061A1
GENERAL INFORMATION:
APPLICANT: Utansky, Samuel
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,474
FILING DATE: 14-MAY-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5500
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 685 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

Query Match 62.9%; Score 823.5; DB 9; Length 685;
Best Local Similarity 60.0%; Pred. No. 3e-58; Mismatches 39; Indels 43; Gaps 8;
Matches 159; Conservative 24; MisMatches 39; Indels 43; Gaps 8;

Qy 11 SLL-LLLAQVGRAAAASKAPKVCQETTVPMRGIGNLTHMPNQFNHDTOEAGLEVH 68
Db 11 SLLAALAVLQRSSGAAASAKELACOBITVPLCKGIGNYTIPMPNQFNHDTOEAGLEVH 70

Qy 69 QWPMLVEIQCSPLRFLFLCTMYPICLDPYKHLPLPPCRSVERAKAGCSPLMRQGFAMP 128
Db 71 QWPMLVEIQCSPLDKFLCLSMYTPICLDPYKHLPLPPCRSVERAKAGCSPLMRQGFAMP 130

Qy 129 ERMSCDLPVLGRDAEVLCMDYRNRSBATA--PPRPPAKTLPG-----PPG 174
Db 131 DRMRCDLPLEQG-NPDTLCMDYRNRTDUTAAPSPRRRLPPPP-PGEQPPSGHSRPPG 188

Qy 175 A-----PASGGEC--PAGGPFY---CKCREPPVPLIKESHPLYNK 209
Db 189 APPHRGGSSRGDDAAAPPSRGKKARPPIGGAAACCEPGCOCRAPMVSVSSERHPLYNR 248

Qy 210 VRTGQVNCAVPCYQPSFSADERTF 234
Db 249 VKTGQIANCALPCNPPFSQDERAF 273

RESULT 11
US-09-847-102A-57
Sequence 57, Application US/09847102A
Publication No. US20030044409A1
GENERAL INFORMATION:
APPLICANT: University of California
APPLICANT: Carlson, Dennis A.
APPLICANT: Corr, Maritat
APPLICANT: Rhee, Chae-Seo
APPLICANT: Lorenzo, Leon M.
APPLICANT: Malini, Sen
TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
FILE REFERENCE: 22000-20629_00
CURRENT APPLICATION NUMBER: US/09/847,102A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 57
LENGTH: 685
TYPE: PRT
ORGANISM: Mouse
US-09-847-102A-57

Query Match 62.9%; Score 823.5; DB 9; Length 685;
Best Local Similarity 60.0%; Pred. No. 3e-58; Mismatches 39; Indels 43; Gaps 8;
Matches 159; Conservative 24; MisMatches 39; Indels 43; Gaps 8;

Qy 11 SLL-LLLAQVGRAAAASKAPKVCQETTVPMRGIGNLTHMPNQFNHDTOEAGLEVH 68
Db 11 SLLAALAVLQRSSGAAASAKELACOBITVPLCKGIGNYTIPMPNQFNHDTOEAGLEVH 70

Qy 69 QWPMLVEIQCSPLRFLFLCTMYPICLDPYKHLPLPPCRSVERAKAGCSPLMRQGFAMP 128
Db 71 QWPMLVEIQCSPLDKFLCLSMYTPICLDPYKHLPLPPCRSVERAKAGCSPLMRQGFAMP 130

Qy 129 ERMSCDLPVLGRDAEVLCMDYRNRSBATA--PPRPPAKTLPG-----PPG 174
Db 131 DRMRCDLPLEQG-NPDTLCMDYRNRTDUTAAPSPRRRLPPPP-PGEQPPSGHSRPPG 188

Qy 175 A-----PASGGEC--PAGGPFY---CKCREPPVPLIKESHPLYNK 209
Db 189 APPHRGGSSRGDDAAAPPSRGKKARPPIGGAAACCEPGCOCRAPMVSVSSERHPLYNR 248

QY 210 VRIGQVPCAVPVCYQQPSFSADETRP 234
 |:|||: |||: | | | |
 ; Sequence 37, Application US/09847102A
 ; Publication No. US2003004409A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of California

RESULT 12
 US-09-847-102A-37
 ; Sequence 37, Application US/09847102A
 ; Publication No. US/09847102A
 ; GENERAL INFORMATION:
 ; APPLICANT: Carson, Dennis A.
 ; APPLICANT: Corr, Maripat
 ; APPLICANT: Lorenzo, Leoni M.

APPLICANT: Malini, Sen
 TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
 FILE REFERENCE: 22000-20629.00
 CURRENT APPLICATION NUMBER: US/09/847,102A
 NUMBER OF SEQ ID NOS: 138
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 37
 LENGTH: 599
 TYPE: PRT
 ORGANISM: Mouse
 US-09-847-102A-37

Query Match 56.5%; Score 740.5; DB 9; Length 599;
 Best local Similarity 60.3%; Pred. No. 1.2e-51; Matches 146; Conservative 20; Mismatches 43; Indels 33; Gaps 7;
 QY 11 SLL--LILIAQLYGRVAAASKAPVCPQEITVPMRGIGNLTHMPQENHDTDEAGLEVH 68
 Db 11 SLILALAVIQLRQSSCAAASKAKELACQETIVPLCKGIGNYTAMPNQENHDTDEAGLEVH 70
 QY 69 QFWPLVETIQCSPLDRFLCTMTPICLDPYKLPCLPCRSVERAKAGCSPLMRQYGFAMP 128
 Db 71 QFWPLVETIQCSPLDKFLPKLCMYTPICLEDYKPKLPLCPVCERAKAGCPLMRQYGFAMP 130
 QY 129 ERMSCDRLPLVLGRDAEVLCMDYRTEAAPSPPRRLPPPP-PGEQPPSGSGHSRPPG 188
 Db 131 DRMECDRLPLQEQG-NFTLQMDYRTEAAPSPPRRLPPPP-PGEQPPSGSGHSRPPG 188
 QY 175 A--PASGERCPASGERCPVVKCREPFPVILKESHLPLYNKVYRTGQPNCAVPCYQOSFFSADE 232
 Db 189 ARPFRGGSSRGSSGD-----AAAAPPSRGKGIGQFANCALPCHNFFSQDER 235
 QY 233 TF 234
 Db 236 AF 237

RESULT 13
 US-10-152-548-2
 Query Match 47.4%; Score 621; DB 9; Length 694;
 Best Local Similarity 43.4%; Pred. No. 5.1e-42; Matches 124; Conservative 27; Mismatches 55; Indels 80; Gaps 7;
 QY 22 GRAAASKAP-----VCOBITVPCRGIGNLTHMPQENHDTDEAGLEVH 68
 Db 40 GHGLDASPAAPGVGPATPKDPNLRCEBTTFCRGIGNYTAMPNQENHDTDEAGLEVH 99
 QY 69 QFWPLVETIQCSPLDRFLCTMTPICLDPYKLPCLPCRSVERAKAGCSPLMRQYGFAMP 128
 Db 100 QFWPLVETIQCSPLDKFLPKLCMYTPICLEDYKPKLPLCPVCERAKAGCSPLMRQYGFAMP 159
 QY 129 ERMSCDRLPLVLGRDAEVLCMDY-----
 Db 160 ERMACERPLHGS-DPDNLCMEGPSVTAEGSGGGGGGGGGKRKQGGSGSGGS 218
 QY 151 ----NRSEATTPRPFPAKPTLPGPPGAPASGGEC-PAGGPFPVVKCREPYV----- 197
 Db 219 GAGGSSGSTSTPKCRGRNSK-NCQNPOGEKAQSKGECS----CSCRSPLFLGKEQOLLQ 271
 QY 198 ----PLKESHLPLYNKVY--RTGQPNCAVPCYQOSFFSADERTFA 235
 Db 272 QQSOPMMHHPHWYMLTVORIAGVENCGBCKGPPFSNDBKDF 317

RESULT 14
 US-09-847-102A-43
 ; Sequence 43, Application US/09847102A
 ; Publication No. US2003004409A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of California
 ; APPLICANT: Carson, Dennis A.
 ; APPLICANT: Corr, Maripat
 ; APPLICANT: Lorenzo, Leoni M.
 ; APPLICANT: Nurse, Roel
 TITLE OF INVENTION: Wnt Receptor Compositions and Methods
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Delinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto

; APPLICANT: Malini Sen
; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
; STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
; FILE REFERENCE: 22000-20629_00
; CURRENT APPLICATION NUMBER: US/09/847,102A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Drosophila
; US-09-847-102a-43

Query Match
Best Local Similarity 44.7%; Score 585; DB 9; Length 570;
Matches 117; Conservative 25; Mismatches 52; Indels 48; Gaps 6;
Qy 22 GRRAAAASKAP-----VCOETVPMCRGIGYNLTIMPNOHNHDDEAGLEHV 68
Db 29 GHGLDASPAAGPYGVPAIPKDPNLRCEHFRHG--AEQICVGQNHSEDGAPALTTAPP--PGLQPG 175
Qy 69 QWMPVLVEIQCSIDLRLFFLCTMTPICLDYHKPLPPRSVCERAKAGSPLMRQYGRAMP 128
Db 89 QWPWPLVIEIKCSIDLKLFLCSMVTPICLDYHKPLPPRSVCERAKAGSPLMRQYGRAMP 148
Qy 129 ERMSCDRLPVLGDAEVLCMDY-NRSEATTAPPRPFPAKPTLPGPGRAPASG----- 179
Db 149 ERMACERHLPLHG-DPDNLCLMEQPSYTERAGSGGS-----SGGGGGGGGGKKR 198
Qy 180 -----GRCPAGGPFVCKCREPPVPLIKESHPLYNKRTGQVNCAVPCYQPSFSADERT 233
Db 199 QGGSGSGSGGSSGS-----TSTKPCRGORIAGYVNGCNGGIPCKGPPFSNDEKD 248
Qy 234 FA 235
Db 249 FA 250

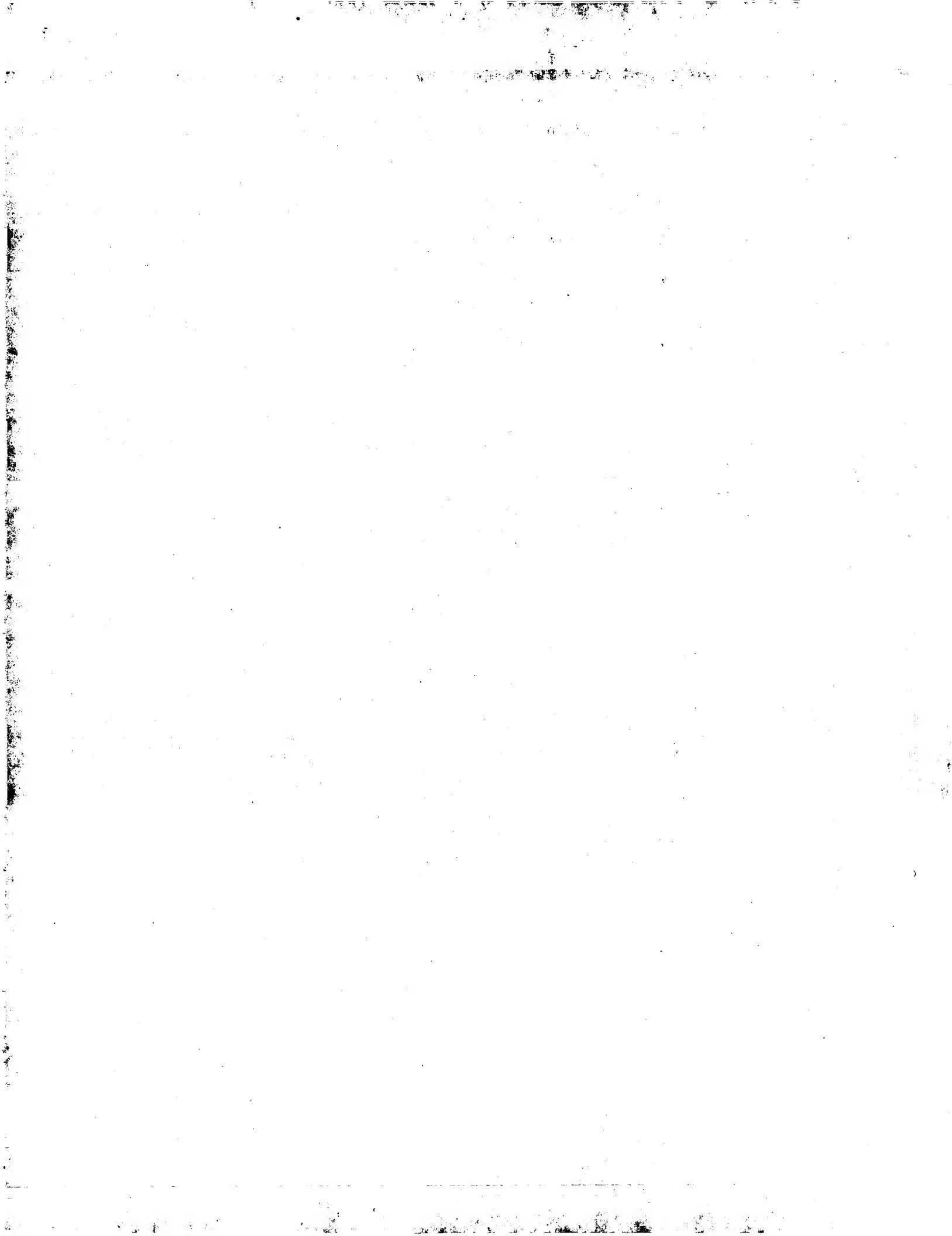
RESULT 15

US-09-847-102a-63
; Sequence 63, Application US/09/847-102a
; Publication No. US20030104409A1
; GENERAL INFORMATION:
; APPLICANT: University of California
; APPLICANT: Carson, Dennis A.
; APPLICANT: Corri, Maripat
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Lorenzo, Leoni M.
; APPLICANT: Malini, Sen
; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
; STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
; FILE REFERENCE: 22000-20629_00
; CURRENT APPLICATION NUMBER: US/09/847,102A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-847-102a-63

Query Match 36.4%; Score 477; DB 9; Length 244;
Best Local Similarity 41.9%; Pred. No. 5.8e-31; Mismatches 79; Indels 40; Gaps 11;
Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;
Qy 3 RPDPAPSPLLLLAQLVGRRAAAASKAPV-----VCOETVPMCRGIGYNLTIMPNOHF 55
Db 2 RPRSPALPRLPLLPPLAAGPAIPFGKGKISIPDHGFQOPTSIPCLTDIAVNTOIMPNLL 61
Qy 56 NHDTQDEAGLEHVQWMPVLVEIQCSIDLRLFFLCTMTPICLDYHKPLPPRSVCERAKAG 115

Do 62 GHTNQEDAGLEHVQWMPVLVKYCSPBLRFIFCSMYAPVCTV-LEQIIPPCRICERAROG 120
Qy 116 CSPLMRYGFAWPERMSCDRLPVLGLRDAEVLCMDYDNRSE---ATTAPRPFPA-KPT 168
Do 121 CRALMNKFGFQMPERLURCEHFRHG--AEQICVGQNHSEDGAPALTTAPP--PGLQPG 175
Qy 169 LPGPPGAPASCBCPAGG---PPVCKCRELPPVPIKESHLYNKRTGQVNCAVPCYQ 224
Do 176 AGTPGGGGCAAPPVATELHPFHCP----RVLKV--PSYLSYKFLGRDCAAPC-E 226
Qy 225 PS-----FSADERTFA 235
Do 227 PARPDGSMFFSQEETREA 244

Search completed: May 19, 2003, 16:43:39
Job time : 25 secB



GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 16:32:41 ; Search time 20 Seconds
(without alignments)

1129.579 Million cell updates/sec

Title: US-09-847-102a-68
Perfect score: 1310
Sequence: 1 MARPDPAPPSSULLLAAQL.....PNCAVPCYQPSFSADERTFA 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73;*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	621	47.4	694	2	S71786 wingless receptor
2	477	36.4	565	2	JB0338 Frizzled-2 protein
3	461	35.2	574	2	JB0339 Frizzled-7 protein
4	451	34.4	550	2	T37325 wingless protein r
5	415	31.7	647	2	JB0337 Frizzled-1 protein
6	399	30.5	641	2	A45054 probable intercell
7	384	29.3	581	2	JC7086 FZD10 protein - hu
8	370.5	28.3	581	2	S93540 gene frizzled prot
9	366.5	28.0	605	2	T31690 hypothetical prote
10	339.5	25.9	568	2	T25162 frizzled-1 protein
11	334	25.5	197	2	JCT735 frizzled-related p
12	308	23.5	537	2	JC7127 frizzled protein 4
13	297	22.7	666	2	JC7312 frizzled-3 protein
14	282	21.5	706	2	JB0164 frizzled-6 protein
15	270.5	20.6	295	2	JR0174 frizzled protein-2
16	270	20.6	317	2	JR0175 frizzled protein-1
17	218.5	16.7	1113	2	JB0315 low-density lipop
18	170	13.0	579	2	JC7629 membrane-type friz
19	161.5	12.3	526	2	T13484 frizzled protein h
20	140.5	10.7	1774	2	BB6101 collagen alpha 1(X)
21	127.5	9.7	793	2	JG5539 smoothend protein
22	106.5	8.1	1955	1	AGCH agrin precursor -
23	98.5	7.5	768	2	AB7722 protein ZC123.1
24	96.5	7.4	211	2	B9716 protein F5B8.3
25	96.5	7.4	241	2	T2216 hypothetical prote
26	94.5	7.3	1428	2	TU8852 lustrin A - Calflo
27	94.5	7.2	HT5253 hypothetical prote		
28	93	7.1	871	1	IAB696 protein-tyrosine k
29	93	7.1	148697		protein-tyrosine k
31	92.5	7.1	1464	2	S59856 collagen alpha 1(I
32	92	7.0	1464	1	C9HULS zinc finger protei
33	91.5	7.0	303	2	T28999 collagen alpha 1(I
34	90	6.9	488	2	A27353 hypothetical prote
35	90	6.9	1221	2	A49457 collagen alpha 1(I
36	89.5	6.8	674	2	S13301 fibulin-2 precursor
37	88.5	6.8	196	2	A48150 hibernation-relate
38	88.5	6.8	316	2	T31880 hypothetical prote
39	88	6.7	215	2	B48150 hibernation-relate
40	87.5	6.7	375	2	T16248 hypothetical prote
41	87.5	6.7	396	1	KXBOZ plasma protein Z -
42	87	6.6	510	1	S43692 transcription fact
43	86.5	6.6	346	2	T01123 hypothetical prote
44	86.5	6.6	700	2	D75508 serine/threonine P
45	86	6.6	289	2	S55667 thymidylate synthase

ALIGNMENTS

RESULT 1
S71786 wingless receptor precursor dfz2 - fruit fly (*Drosophila melanogaster*)
C;Species: *Drosophila melanogaster*
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 02-Mar-2001
C;Accession: S71786; S78444
R;Bhanot, P.; Brink, M.; Harryman Samos, C.; Hsieh, J.C.; Wang, Y.; Macke, J.P.; Andrew, A;Title: A new member of the frizzled family from *Drosophila* functions as a wingless rec
A;Reference number: S71786; MUID:96353971; PMID:8717036
A;Accession: S71786
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-694 <BHA>
A;Cross-references: EMBL:U65589; NID:91518050; PIDN: AAC47273.1; PID:91518051
A;Genetic: dtz2
A;Gene: dtz2
A;Cross-references: Flybase:FBgn0016797
A;Superfamily: fruit fly frizzled protein
C;Keywords: transmembrane protein

Query Match 47.4%; Score 621; DB 2; Length 694;
Best Local Similarity 43.4%; Pred. No. 6.6e-42;
Matches 124; Conservative 27; Mismatches 55; Indels 80; Gaps 7;
C;Keywords: transmembrane protein

Qy 22 GRAMAAASKP-----VQEITWPMERGIGNLTHMNPQHDTQDAGLEH 68
Db 40 GHGLDASPAQGYVPAIKDPPNLRCEETIPMCRGIGYNTSPNEMHETQDAGLEH 99

Qy 69 QFWPLVEIQCSDPDRFLCTMYKPICLPDYKHPPLPPCSVCERAKAGSPLMROYFAMP 128
Db 100 QFWPLVEIKCSDPKFLCSMVTICLEDYHKPLPVCSVCERASGCAPIMQYSFEMP 159

Qy 129 ERMSCDRLPVGLGRDAEVLCMDY----- 150
Db 160 ERMACEHULHDG-DPDNLCMEQPSYTEAGSGGGGGGGGGGGKKQQGGGGGS 218

Qy 151 ---NRSEATTPRPRPKPTLPGPGPAPASCGCPCAGPFVCKCRSPFV----- 197
Db 219 GAGGSSGSTSTKPCRGNSK-NCNPOQGERASGRCES---CSCRSPLIFLGKEQLLQ 271

Qy 198 ---PLIKESPLINKV---RTQVQVNCAPCQPSFSADERTFA 235
Db 272 QSQSMQMMHHPHWYMNLTQRIAGVPGNGCICKGPPFSNDKDFA 317

RESULT 2
Frizzled-2 protein - human
C;Species: Homo sapiens (man)

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001
C;Accession: JE0338
R;Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.

A;Title: Molecular cloning, differential expression, and chromosomal localization of hum
A;Reference number: JB0337; MUID:99032814; PMID:9813155

A;Accession: JE0338
A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-565 <SG>

A;Cross-references: DDBJ:AB017364; NID:93927884; PIDN:BAA34667.1; PID:93927885

C;Superfamily: fruit fly frizzled protein

Query Match 36.4%; Score 477; DB 2; Length 565;
Best Local Similarity 41.9%; Pred. No. 1.5e-30;
Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

Qy 3 RPDPSADPSLILLLAQOLVGRAAAASKAPV-----CQEITVPMRGIGINLNTHMPNQF 55
Db 2 RPRSALEPRLLFLILLPAAGPAPQFHGEGKGSISPDHGRCQPISPICLTDIAVNOTIMPNL 61

Qy 56 NHDTDQEAGLEPHOFWLVQOCSPDRLFFCTMYPICLFDYHKQLPPCSVCERAKAG 115
Db 62 GHTNQEBAGLEPHOFWLVQOCSPDRLFFCTMYPICLFDYHKQLPPCSVCERAKAG 120

Qy 116 CSPLMROYGFAPERMSCDRULPVGRDAEVLCDMDYRSE----ATTAPRPFPA-KPT 168
Db 121 CEAALMNKEFGQPERLRCHEFFRHG--AEQICVGQHNSEDGAPALLTAPP---RGLQPG 175

Qy 169 LPGPPGAPASGGCCPAGG---PFCVKCREEPVVPLIKESHPLYNKRTGQIVPNCAVPCYQ 224
Db 176 AGGTGCGPGGGGAPPRVATLEHPFHCP----RVLKVV- PSYLSVKGFLGERDCAAPC-E 226

Qy 225 PS-----FSADERTPA 235
Db 227 PARPDGSMWFFSOEBTRPA 244

RESULT 3
Frizzled-7 protein - human
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001
C;Accession: JE0339
R;Sagara, N.; Ioda, G.; Hirai, M.; Terada, M.; Katoh, M.
Biochem. Biophys. Res. Commun. 252, 117-122, 1998
A;Title: Molecular cloning, differential expression, and chromosomal localization of hum
A;Reference number: JB0337; MUID:99032814; PMID:9813155

A;Accession: JE0339
A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-574 <SG>

A;Cross-references: DDBJ:AB017365; NID:93927886; PIDN:BAA34668.1; PID:93927887

C;Superfamily: fruit fly frizzled protein

Query Match 35.2%; Score 461; DB 2; Length 574;
Best Local Similarity 40.1%; Pred. No. 2.9e-29; Mismatches 81; Indels 46; Gaps 12;

Qy 1 MARPDPSAPS--LILLLAQOLVGRAAAASKAPV-----VCQEITVPMRGII 44
Db 1 MRDPGAAPLASSLGLCALVNLALGALSAGAGQPHGEGKGSISPDHGRCQPISPICLTDI 60

Qy 45 GYNLTIPMNPQFNHDTEAGLEPHOFWLVQOCSPDRLFFCTMYPICLFDYHKPLPP 104
Db 61 AYNTQTLIPNLIGHTNODAGLEPHOFWLVQOCSPDRLFFCTMYPICLFDYHKPLPP 119

RESULT 4
wingless protein receptor Cfz2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Mar-2001
C;Accession: T37325
R;Sato, A.; Kojima, T.; Ui-Tej, K.; Miyata, Y.; Saigo, K.
Development. 126, 4421-4430, 1999
A;Title: Dfrizzled-3, a new *Drosophila* Wnt receptor, acting as an attenuator of Wingless
A;Reference number: T21669; MUID:99429803; PMID:10498678

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-550 <RT>

A;Genetic:

A;Gene: Cfz2

C;Superfamily: fruit fly frizzled protein

C;Keywords: receptor; signal transduction; transmembrane protein

Query Match 34.4%; Score 451; DB 2; Length 550;
Best Local Similarity 38.9%; Pred. No. 1.7e-28; Mismatches 77; Indels 38; Gaps 6;

Qy 11 SILLILAQOLVGRAAAASKAPVQCBITVPMRGIGYNLNTHMPNQFNHDTEAGLEPHOF 70
Db 6 SVFLFLIGSC--GALFGKRKCEOTIPLCKGIGYNMTSPNSYGHKEKOBEGLEHVOF 62

Qy 71 WFLVETQCSPLDRFLCTMYPICLFDYHKPLPPORSVERAKAGCSPLMRQKGAWPER 130
Db 63 YPLVVEGCFQHLKFLCTMYPICLFDYHKPLPPORSVERAKAGCSPLMRQKGAWPER 122

Qy 131 NSCDRLULPVLSRDAEVLCMDYRSEATTAPRPFPAKP-----TLPG 171

Db 123 ISCEALPKMG-----DQNSIGNICAAPPDPITKKHQKHKKHQNQNQHQHNHYSPDG 174

Qy 172 PP-GAPASGCCPAG-GPYVKCREEPVVPLIKESHPLYNKRTGQIVPNCAVPCYQSF 228
Db 175 PEGVSKIDNEVIAGPSECQTCNQPFQVASE----RSKVGNVTNCAYSSCHSPALA 227

RESULT 5
Frizzled-1 protein - human
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001
C;Accession: JE0337
R;Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.
Biochem. Biophys. Res. Commun. 252, 117-122, 1998
A;Title: Molecular cloning, differential expression, and chromosomal localization of hum
A;Reference number: JE0337; MUID:99032814; PMID:9813155

A;Accession: JE0337

A;Molecule type: mRNA

A;Residues: 1-647 <SG>

A;Cross-references: DDBJ:AB017363; NID:93927882; PIDN:BAA34666.1; PID:93927883

C;Superfamily: fruit fly frizzled protein

Query Match 31.7%; Score 415; DB 2; Length 647;

Best Local Similarity 36.0%; Pred. No. 1.5e-25;

Db 169 ---DCKHLSPPDRCKCK 182

RESULT 12

C;Species: Homo sapiens (man)
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
C;Accession: JC7127
R;Kirikoshi, H.; Sagara, N.; Koike, J.; Tanaka, K.; Sekihara, H.; Hirai, M.; Katoh, M.
Biotech. Biophys. Res. Commun. 264, 955-961, 1999
A;Title: Molecular cloning and characterization of human frizzled-4 on chromosome 11q14-
A;Accession: JC7127
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-537 <KIR>
A;Cross-references: GB:AB032417; DDBJ:AB032417; NID:96277265; PID:96277266
C;Genetics:
A;Gene: FZD4
A;Map position: 11 region q14 - q21
C;Superfamily: fruit fly frizzled protein

Query Match 23.5%; Score 308; DB 2; Length 537;
Best Local Similarity 34.0%; Pred. No. 4e-17; Mismatches 71; Indels 20; Gaps 5;
Matches 64; Conservative 33; Mismatches 64;

Qy 6 PSAPPRL---LILLAQIYG--RAAAASKAPVCOEITPMCRGIGYNTTHMPQFNHD 58

Db 11 PGAPGGVGSLGLLQLLQLLQGPARGFGEDEERRCDPIRISMCOQLYNNTKMPNLVGE 70

Qy 59 TQDEAGLEVHQFWPLVLEIQSPDPLRFLLCTMYTPICLDPYKPLPPCRSVCEAKAGCSP 118

Db 71 LQTDSLQLTTPFLQYQGSSQLQFLCSYVUPMCTEKINIPICPGGMQLSVERCEP 130

Qy 119 IMRQXCPAWPRMWCURLPVLGRDAVFLCMYNRSAATTAPPRFAKPTLPGPPGAPAS 178

Db 131 VLKEFGFAWPESLNQSKFPP-QNDHNHNCMEGPQDVEVPLPHKT-PIQ----- 177

Qy 179 GGECPAGG 186

Db 178 GEECHSVD 185

RESULT 13

JC7312

frizzled-3 protein - human
C;Species: Homo sapiens (man)
C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 02-Mar-2001
C;Accession: JC7312
R;Sala, C.F.; Formenti, E.; Terstappen, G.C.; Caricasole, A.
Biotech. Biophys. Res. Commun. 273, 27-34, 2000
A;Title: Identification, gene structure, and expression of human frizzled-3 (FZD3).
A;Reference number: JC7312
A;Accession: JC7312
A;Molecule type: mRNA
A;Residues: 1-666 <SAL>
A;Cross-references: GB:AB27242
A;Experimental source: brain
C;Comment: This protein, a seven-transmembrane receptor belonging to the frizzled family
C;Genetics:
A;Gene: fzd3
A;Map position: 8p21
C;Superfamily: fruit fly frizzled protein
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 21.5%; Score 282; DB 2; Length 706;
Best Local Similarity 30.8%; Pred. No. 6.1e-15; Mismatches 65; Indels 44; Gaps 6;
Matches 65; Conservative 22; Mismatches 65;

Qy 33 QOBETVPMCRGIGYNTTHMPQFNHD TQDEAGLEVHQFWPLVLEIQSPDPLRFLLCTMYTP 92

Db 24 CEPITVPRCRMAYMVNTFPFLMGHYSIAVEMEHFLPLANECSPRIETFLCKAFV 83

Qy 93 ICLPDYHKPKUPCRSVCEAKAGSPLMQLQYGFPAWERMSCDRFLVSLGRDAEVLCMDYR 152

Db 84 TCIEQIH-WVPCRKLCERKVSYDSKLLIDTFGIRWPEELCDRLQYCDETVPV----- 135

Qy 153 SEATTAAPPRE--PAKPTLPGPPGAPASGCGCPAGGPVYCKCREPPVPLKESHLINKV 210

Db 136 ---TDFPHTFLGPROKT-----EQVORDIGFWC-----PRHLKT 167

Qy 211 RTGO-----VPMCAVPCIQPSFSADERFTA 235

Db 168 SGGQEVKFLIDQCAPCPMIVFKSDLEPA 198

RESULT 14

JE0164

frizzled-6 protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 01-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 02-Mar-2001
C;Accession: JE0164
R;Tokuhara, M.; Hirai, M.; Atomi, Y.; Terada, M.; Katoh, M.
Biotech. Biophys. Res. Commun. 243, 622-627, 1998
A;Title: Molecular cloning of human frizzled-6.
A;Reference number: JE0164; MUID:98153814; PMID:9480858
A;Molecule type: mRNA
A;Residues: 1-706 <TOX>
A;Cross-references: GB:AB012911; NID:93062802; PID:93062803
C;Comment: This protein is receptor for selected glycoproteins in development and carcinogenesis:
A;Gene: Hizz6
A;Map position: 8q22.3-q23.1
C;Superfamily: fruit fly frizzled protein
C;Keywords: glycoprotein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;201-222/Domain: transmembrane #status predicted <TM1>
F;233-255/Domain: transmembrane #status predicted <TM2>
F;281-312/Domain: transmembrane #status predicted <TM3>
F;324-345/Domain: transmembrane #status predicted <TM4>
F;370-393/Domain: transmembrane #status predicted <TM5>
F;417-436/Domain: transmembrane #status predicted <TM6>
F;473-495/Domain: transmembrane #status predicted <TM7>
F;38,352/Binding site: carbohydrate #status predicted (covalent) #status predicted
F;38,352/

RESULT 15

JE0174

frizzled protein-2 - human
C;Species: Homo sapiens (man)
C;Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999
C;Accession: JE0174

R;Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.
Biochem. Biophys. Res. Commun. 247, 287-293, 1998
A;Tissue: tissue restricted expression of two human frzb genes in preadipocytes and pancreas.
A;Reference number: JE0174; MUID:98308108; PMID:9642118

A;Accession: JE0174
A;Molecule type: mRNA
A;Residues: 1-295 <HUA>

C;Genetics:
A;Map position: 4q

Query Match Score 270.5; DB 2; length 295;
Best Local Similarity 20.6%; Prod. No. 2.2e-14;
Matches 62; Conservative 26; Mismatches 60; Indels 23; Gaps 7;
Qy 9 PSSLLLILAQ-----LVGRAAAASKAPVCOBI-TVPMCRRGIGYMLTHMPNQF 55
Db 5 PSSLLLFLFLASHCCLGSARGRLFLFGQDFPSYKRSNCKPAPIANLQLCHGIEYQNMRLPNLL 64
Qy 56 NNDTODAGLEPHQFW-PVLFETQSPDLRFELCTMYPPICLDYKOLPPRSVCERAKA 114
Db 65 GHBTMKEV-LEQAGAWIPLVMKQCHPDTKKFLCSLFAVCLDDETIQPCHSILCVQVKD 123
Qy 115 GSPLMLRQYFAMPERNSCDRIPVLRGDAEVLCMDYRSE---ATTAPPR 161
Db 124 RCAPVMSAFGFPPWPDMLECDRFP--QDND-LCIPLASSDHLLPATEEAPR 170

Search completed: May 19, 2003, 16:34:58
Job time : 24 secs

GenCore version 5.1.4_ps_4578
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OM: protein - protein search, using sw model

Run on: May 19, 2003, 16:32:11 ; Search time 13 Seconds
 (without alignments)
 749.764 Million cell updates/sec

Title: US-09-847-102a-68
 Perfect score: 1310
 Sequence: 1 MARPDPAPPSSULLLAQL.....PNCAVPCYQPSFSADERTPA 235

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1310	100.0	585	1 FZD5_HUMAN	Q13467 homo sapien
2	1143	87.3	577	1 FZD5_MOUSE	Q9eqdd mus musculus
3	825.4	63.0	559	1 FZD5_XENIA	P58421 xenopus laevis
4	824.5	62.9	694	1 FZD8_HUMAN	Q9h461 homo sapien
5	823.5	62.9	685	1 FZD8_MOUSE	Q61091 mus musculus
6	802	61.2	581	1 FZD8_XENIA	Q93274 xenopus laevis
7	621	47.4	694	1 FZD2_DROME	Q9vvx3 drosophila melanogaster
8	477	36.4	565	1 FZD2_HUMAN	Q14332 homo sapien
9	476	36.3	570	1 FZD2_MOUSE	Q9jps6 mus musculus
10	35.6	46.6	570	1 FZD2_RAT	Q08464 rattus norvegicus
11	45.7	34.9	574	1 FZD7_HUMAN	Q75084 homo sapien
12	440.5	33.6	572	1 FZD7_MOUSE	Q61090 mus musculus
13	438.5	33.5	551	1 FZD2_XENIA	Q9puu5 xenopus laevis
14	431	32.9	592	1 FZD1_CHICK	Q57328 gallus gallus
15	422	32.2	642	1 FZD1_MOUSE	Q70421 mus musculus
16	421	32.1	523	1 FZD2_CHICK	Q9ia05 gallus gallus
17	414.5	31.6	648	1 FZD1_HUMAN	Q9up38 homo sapien
18	411	31.4	567	1 FZD7_CHICK	Q57329 gallus gallus
19	405.5	31.0	547	1 FZD7_XENIA	Q9puu5 xenopus laevis
20	401	30.6	559	1 FZD1_XENIA	Q919m5 xenopus laevis
21	398	30.4	641	1 FZD1_RAT	Q08463 rattus norvegicus
22	394.5	30.1	591	1 FZD7_HUMAN	Q00144 homo sapien
23	394.5	30.1	592	1 FZD9_MOUSE	Q9r215 mus musculus
24	384	29.3	581	1 FZD10_HUMAN	Q9qlw2 homo sapien
25	372	28.4	576	1 FRIZB_HUMAN	Q92765 homo sapien
26	371	28.3	583	1 FRIZB_DROS	Q24760 drosophila melanogaster
27	370.5	28.3	581	1 FRIZB_DROME	P18537 drosophila melanogaster
28	368	28.1	581	1 FRIZB_XENIA	Q9debs xenopus laevis
29	367	28.0	323	1 FRIZB_MOUSE	P97401 mus musculus
30	366	27.9	325	1 FRIZB_BOVIN	Q95117 bos taurus
31	360	27.5	580	1 FRIZB_XENIA	Q9w742 xenopus laevis
32	351	26.8	585	1 FRIZB_CHICK	CC
33	351	26.8	1	FZD4_XENIA	Q9z319 mus musculus
34	30.8	23.5	537	1 FZD4_HUMAN	O9ulvi homo sapien
35	304.5	23.2	666	1 FZD3_MOUSE	Q61085 mus musculus
36	302.5	23.1	525	1 FZD4_CHICK	Q9ia05 gallus gallus
37	300.5	22.9	538	1 FZD4_RAT	Q9qzho ratus norvegicus
38	299.5	22.9	537	1 FZD4_MOUSE	Q61086 mus musculus
39	297	22.7	666	1 FZD3_HUMAN	Q9npg1 homo sapien
40	293.5	22.4	664	1 FZD3_DROME	Q92579 xenopus laevis
41	284	21.7	705	1 FZD4_DROME	Q9bw1 drosophila melanogaster
42	282	21.5	706	1 FZD6_HUMAN	Q60353 homo sapien
43	271	20.7	709	1 FZD6_MOUSE	Q61089 mus musculus
44	261	19.9	581	1 FZD3_DROME	Q97438 drosophila melanogaster
45	218.5	16.7	1113	1 CORI_MOUSE	Q9z319 mus musculus

ALIGNMENTS

RESULT 1
 FZD5_HUMAN STANDARD; PRT; 585 AA.
 PZD5_HUMAN [2]
 AC Q13467;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled 5 precursor (Frizzled-5) (Fz-5) (FZE5).
 RT FZD5 OR HZ5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A.
 RP RC
 RN TISSUE=Retina;
 RX MEDLINE=96224032; PubMed=8626800;
 RA Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.; "A large family of putative transmembrane receptors homologous to the product of the Drosophila tissue-polarity gene frizzled.";
 RL J. Biol. Chem. 271:4468-4476(1996).
 RN [2] SEQUENCE FROM N.A.
 RP MEDLINE=21301556; PubMed=11408929;
 RX Saitoh T., Hirai M., Katch M.; "Molecular cloning and characterization of human Frizzled-5 gene on chromosome 2q31.3-q34 region.";
 RT Chromosome 2q31.3-q34 region.
 RL Int. J. Oncol. 19:105-110(2001).
 RN [3] SEQUENCE OF 273-331 FROM N.A.
 RP TISSUE=Oesophageal carcinoma;
 RX MEDLINE=98374371; PubMed=9707618;
 RA Tanaka S., Akiyoshi T., Mori M., Wands J.R., Sugimachi K.; "A novel frizzled gene identified in human esophageal carcinoma mediates APC/beta-catenin signals.";
 RT Proc. Natl. Acad. Sci. U.S.A. 95:10164-10169(1998).
 RL [4] COUPLING TO BETA-CATENIN PATHWAY
 RX MEDLINE=9720741; PubMed=9053360;
 RA He X., Saint-Jeannet J.P., Wang Y., Nathans J., Dawid I., Varmus H.; "A member of the Frizzled protein family mediating axis induction by Wnt-1.";
 RT Wnt-1. Science 275:1652-1654 (1997).
 RL "Science 275:1652-1654 (1997)."
 CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interaction with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated

CC	tissues. Interacts specifically with Wnt5A to induce the beta-catenin pathway.	CC	tissues. Integral membrane protein.
-!- SUBCELLULAR LOCATION: Integral membrane protein.	-!- DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).	Qy	121 ROYGRPAWPERMCDRLPLVGRDAEVLCDMYNRSSEATTAAPRPFRAKPTLPGPGAPASGG 180
-!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).	-!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).	Db	121 ROYGRPAWPERMCDRLPLVGRDAEVLCDMYNRSSEATTAAPRPFRAKPTLPGPGAPASGG 180
-!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.	-!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.	Qy	181 ECPAGGPFVCKCREPFPVPLKESPLYNKRTGQVNCAPVCPYQPSFADERTFA 235
CC	-!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.	Db	181 ECPAGGPFVCKCREPFPVPLKESPLYNKRTGQVNCAPVCPYQPSFADERTFA 235
CC	. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC	.
CC	InterPro: IPR00024; Fz_domain.	CC	InterPro: IPR00024; Fz_domain.
DR	EMBL: U43318; RAC50385.1; --.	DR	EMBL: AB043702; BAB60959.1; --.
DR	Genew; HGNC:4043; FZDS.	DR	Genew; HGNC:4043; FZDS.
DR	MIM: 601723; --.	DR	MIM: 601723; --.
DR	InterPro: IPR000539; Frizzled.	DR	InterPro: IPR000539; Frizzled.
DR	PRINTS: PR00489; FRIZZLED.	DR	PRINTS: PR00489; FRIZZLED.
DR	SMART: SM0063; FRI; 1.	DR	SMART: SM0063; FRI; 1.
DR	PROSITE: PS50038; FZ; 1.	DR	PROSITE: PS50038; FZ; 1.
DR	MULIGENE_FAMILY: G-protein_coupled_receptor; Transmembrane; Developmental_protein; Glycoprotein; Signal.	DR	MULIGENE_FAMILY: G-protein_coupled_receptor; Transmembrane; Developmental_protein; Glycoprotein; Signal.
FT	CHAIN 1 26 SIGNAL 1 26 POTENTIAL.	FT	CHAIN 1 26 SIGNAL 1 26 POTENTIAL.
FT	DOMAIN 27 238 FRIZZLED 5.	FT	DOMAIN 27 238 FRIZZLED 5.
FT	TRANSMEM 239 259 EXTRACELLULAR (POTENTIAL).	FT	TRANSMEM 239 259 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 260 270 CYTOPLASMIC (POTENTIAL).	FT	TRANSMEM 260 270 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 271 291 2 (POTENTIAL).	FT	TRANSMEM 271 291 2 (POTENTIAL).
FT	TRANSMEM 292 315 EXTRACELLULAR (POTENTIAL).	FT	TRANSMEM 292 315 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 316 336 3 (POTENTIAL).	FT	TRANSMEM 316 336 3 (POTENTIAL).
FT	TRANSMEM 337 358 CYTOPLASMIC (POTENTIAL).	FT	TRANSMEM 337 358 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 359 379 4 (POTENTIAL).	FT	TRANSMEM 359 379 4 (POTENTIAL).
FT	TRANSMEM 380 402 EXTRACELLULAR (POTENTIAL).	FT	TRANSMEM 380 402 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 403 423 5 (POTENTIAL).	FT	TRANSMEM 403 423 5 (POTENTIAL).
FT	TRANSMEM 424 449 CYTOPLASMIC (POTENTIAL).	FT	TRANSMEM 424 449 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 450 470 6 (POTENTIAL).	FT	TRANSMEM 450 470 6 (POTENTIAL).
FT	TRANSMEM 471 500 EXTRACELLULAR (POTENTIAL).	FT	TRANSMEM 471 500 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 501 521 7 (POTENTIAL).	FT	TRANSMEM 501 521 7 (POTENTIAL).
FT	DOMAIN 522 585 CYTOPLASMIC (POTENTIAL).	FT	DOMAIN 522 585 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 150 150 FZ.	FT	DOMAIN 150 150 FZ.
FT	SITE 525 530 LYS-THR-X-X-X-TRP MOTIF.	FT	SITE 525 530 LYS-THR-X-X-X-TRP MOTIF.
FT	CARBOHYD 47 585 PDZ-BINDING.	FT	CARBOHYD 47 585 PDZ-BINDING.
FT	CARBHYD 151 151 N-LINKED (GlcNAc. . .) (POTENTIAL).	FT	CARBHYD 151 151 N-LINKED (GlcNAc. . .) (POTENTIAL).
FT	CONFLICT 88 88 T -> S (IN REF. 2).	FT	CONFLICT 88 88 T -> S (IN REF. 2).
FT	CONFLICT 262 263 DT -> ER (IN REF. 2).	FT	CONFLICT 262 263 DT -> ER (IN REF. 2).
FT	CONFLICT 345 345 A -> G (IN REF. 2).	FT	CONFLICT 345 345 A -> G (IN REF. 2).
FT	CONFLICT 357 357 G -> A (IN REF. 2).	FT	CONFLICT 357 357 G -> A (IN REF. 2).
FT	CONFLICT 402 402 R -> G (IN REF. 2).	FT	CONFLICT 402 402 R -> G (IN REF. 2).
SQ	SEQUENCE 585 AA; 64551 MW; CF66C5BA746E7971 CRC64;	SQ	SEQUENCE 585 AA; 64551 MW; CF66C5BA746E7971 CRC64;
Query Match	100.0%; Score 1310; DB 1; Length 585;	Query Match	100.0%; Score 1310; DB 1; Length 585;
Best Local Similarity	100.0%; Pred. No. 1.8e-95;	Best Local Similarity	100.0%; Pred. No. 1.8e-95;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-!- TISSUE SPECIFICITY: Expressed in eye, kidney, lung, chondrocytes, epithelial cells of the small intestine and goblet cells of the colon.	CC	-!- TISSUE SPECIFICITY: Expressed in eye, kidney, lung, chondrocytes, epithelial cells of the small intestine and goblet cells of the colon.
CC	-!- DEVELOPMENTAL STAGE: Expressed in the yolk sac, placenta, eye and lung bud at 9.5 days post coitum (dpc). At 10.5 dpc, also expressed in the placental blood vessel of embryonic origin.	CC	-!- DEVELOPMENTAL STAGE: Expressed in the yolk sac, placenta, eye and lung bud at 9.5 days post coitum (dpc). At 10.5 dpc, also expressed in the placental blood vessel of embryonic origin.
CC	-!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).	CC	-!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).
CC	-!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.	CC	-!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.
CC	-!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.	CC	-!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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CC DE 15-JUN-2002 (Rel. 41; last annotation update DT FZ5; Frizzled 5 precursor (Frizzled-5) (FZ-5) (Xf25).

CC GN EMBL; AF272146; AAQ33955.1; - DR Xenopus laevis (African clawed frog).

CC OS MBD; MG1; 108571; Fzds. DR Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Amphibia; Barracuda; Anura; Mesobatrachia; Pipoidea; Pipidae; OC Xenopidae; Xenopus.

CC OC NCBI_TAXID=8355; RN [1]

CC RN PROSITE; PS00038; FZ; 1. DR

CC Pfam; PF0192; Fz; 1. DR

CC Pfam; PF01524; Frizzled; 2. DR

CC PRINTS; PRO0489; FRIZZLED. DR

CC SMART; SMO0063; FRI; 1. DR

CC PROSITE; PS00261; G-PROTEIN RECEP FZ; 4; 1. DR

CC Multi-gene family: G-protein coupled receptor; Transmembrane; Developmental protein; Glycoprotein; Signal. KW SIGNAL 1

CC FT DOMAIN 27 577 DR

CC FT TRANSMEM 27 234 DR

CC FT DOMAIN 235 255 DR

CC FT TRANSMEM 256 266 DR

CC FT DOMAIN 267 287 DR

CC FT TRANSMEM 288 311 DR

CC FT DOMAIN 312 332 DR

CC FT TRANSMEM 333 354 DR

CC FT DOMAIN 355 375 DR

CC FT TRANSMEM 376 398 DR

CC FT DOMAIN 399 419 DR

CC FT TRANSMEM 420 445 DR

CC FT DOMAIN 446 466 DR

CC FT TRANSMEM 467 495 DR

CC FT DOMAIN 496 516 DR

CC FT TRANSMEM 517 577 DR

CC FT DOMAIN 518 150 DR

CC FT SITE 575 577 DR

CC FT CARBOHYD 47 47 DR

CC FT CARBOHYD 151 151 DR

CC SEQUENCE FROM N.A. RN

CC MEDLINE:2123029; PubMed=11335120; RX

CC Sumanas S.; Ekker S.C.; RA "Xenopus frizzled-5: a frizzled family member expressed exclusively in the neural retina of the developing eye."; RT Mech. Dev. 103:133-136(2001).

CC -!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- DEVELOPMENTAL STAGE: First detected at the late neurula stage in retinal primordia. Throughout the tailbud stage, expressed exclusively in the neural retina within the optic vesicles. During tadpole stage, expression becomes restricted to the ciliary marginal zone.

CC -!- DOMAIN: Lys-Tyr-X-X-X-Tp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity). CC -- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).

CC -!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.

CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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CC DE 15-JUN-2002 (Rel. 41; last annotation update DT FZ5; Frizzled 5 precursor (Frizzled-5) (FZ-5) (Xf25).

CC GN EMBL; AR300716; AAK5168.1; - DR

CC InterPro; IPR000539; Frizzled. DR

CC InterPro; IPR000234; Fz domain. DR

CC InterPro; IPR000832; GPCR secretin. DR

CC Pfam; PF01392; Fz; 1. DR

CC Pfam; PF01524; Frizzled; 1. DR

CC PRINTS; PRO0489; FRIZZLED. DR

CC SMART; SMO0063; FRI; 1. DR

CC PROSITE; PS00038; FZ; 4; 1. DR

CC PROSITE; PS00261; G-PROTEIN RECEP FZ; 4; 1. DR

CC Multi-gene family: G-protein coupled receptor; Transmembrane; Developmental protein; Glycoprotein; Signal. KW SIGNAL 1

CC FT CHAIN 27 559 DR

CC FT DOMAIN 27 220 DR

CC FT TRANSMEM 221 241 DR

CC FT DOMAIN 242 257 DR

CC FT TRANSMEM 258 278 DR

CC FT DOMAIN 279 301 DR

CC FT TRANSMEM 302 322 DR

CC FT DOMAIN 323 343 DR

CC FT TRANSMEM 344 364 DR

CC RESULT 3

CC F2D5_XENLA STANDARD; PRT; 559 AA.

CC ID F2D5_XENLA STANDARD; PRT; 559 AA.

CC AC P58421; 15-JUN-2002 (Rel. 41; Created) 15-JUN-2002 (Rel. 41; Last sequence update)

CC DB EC-SGHRVQ--EPFVPLKESHLPLNVRGQVPCAVPCYQPSFSDERTPA 235

CC DB EC-SGHRVQ--EPFVPLKESHLPLNVRGQVPCAVPCYQPSFSDERTPA 231

FT DOMAIN 365 387 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 388 409 5 (POTENTIAL).
 FT DOMAIN 409 434 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 435 455 6 (POTENTIAL).
 FT DOMAIN 456 483 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 484 505 7 (POTENTIAL).
 FT DOMAIN 505 559 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 528 149 FZ. POLY-THR.
 FT SITE 507 512 LYS-THR-X-X-X-TRP MOTIF.
 FT SITE 557 559 PDZ-BINDING.
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 468 559 AA; 63518 MW; 581EB243CB954B7 CRC64;

Query Match 63.0%; Score 825.5; DB 1; length 559;
 Best Local Similarity 69.2%; Pred. No. 1.3e-57;
 Matches 153; Conservative 20; Mismatches 35; Indels 13; Gaps 4;

Oy 14 ILLILQLQVGRAAAASKAPVQCOITVPMCRGIGYNLTHMPNQFNHDDEAGLEVHFWPL 73
 Db 14 VVLLDYFAPAOQASAKAVCQBITVPMCKGIGYNHTMPNQFNHDDEAGMEHVQFWPL 73

Oy 74 VEIQCSDPLREFLCTWTPICLDPYKPLPPCSRVERAKAGCSPNROKGFAWRMSC 133
 Db 74 VVIQCSLDLKFFLCMYTPICLDPYKPLPPCSRVERAKAGCSPNROKGFAWRMNC 133

Oy 134 DRLPVLGRLDAEVICMOMYRNSEATTAPPREPKPTLPGPPGAPASSGECCPAGGPFVCKR 193
 Db 134 DRLPERG-DPDPLCMYNYNTETTTLP-----PTHPKVKRPTS--DCDG---VCKR 180

Oy 194 EPFPVILKEPSHLPLNKVRTGQPNCAVPCYQPSFSADERTF 234
 Db 181 EFPVSIITRESHPLNRYKIKTGQVPCFQPYFTQDERMF 221

RESULT 4

F2DB_HUMAN STANDARD; PRT; 694 AA.

ID F2DB_HUMAN STANDARD; PRT; 694 AA.

DT 09H451; 15-JUN-2002 (Rel. 41, Created)
 15-JUN-2002 (Rel. 41, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)

DE Frizzled 8 precursor (Frizzled-8) (Fz-8) (hFz8).

GN F2DB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_Taxid=9606; [1] RNI MEDLINE=21192958; A. PubMed=11295046; Saitoh T., Hirai M., Katoh M.; "Molecular cloning and characterization of human Frizzled-8 gene on chromosome 10p11.2." Int. J. Oncol. 18:991-996 (2001). [2]

RP SBQUENCE FROM N.A.

RN Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues.

CC -!- SUBCELLULAR LOCATION: Integral membrane Protein.
 CC -!- TISSUE SPECIFICITY: Most abundant in fetal kidney, followed by brain and lung. In adult tissues, expressed in kidney, heart, pancreas and skeletal muscle.

CC -!- DOMAIN: Lys-Thr-X-X-X-TRP motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).
 CC -!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).
 CC -!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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CC DR EMBL: AB043703; BAB1064_1; -.
 DR EMBL: AL121749; CAC10185_1; -.
 DR Genbank: HGNC:4046; FZDB8.
 DR MIM: 606146; -.
 DR InterPro: IPR00539; Frizzled.
 DR InterPro: IPR00024; Fz domain.
 DR InterPro: IPR000832; GPCR_secretin.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF01534; Frizzled; 1.
 DR PRINTS: PR00489; FRIZZLED.
 DR SMART: SM00063; FRI; 1.
 DR PROSITE: PS50201; FZ; 1.
 DR Multigene family; G_protein_coupled_Receptor; Transmembrane; Developmental protein; Glycoprotein; Signal; SIGNAL; 1
 KW FT CHAIN 28 694 FRIZZLED 8.
 FT DOMAIN 28 275 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 276 296 1 (POTENTIAL).
 FT DOMAIN 297 312 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 313 333 2 (POTENTIAL).
 FT DOMAIN 334 396 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 397 417 3 (POTENTIAL).
 FT DOMAIN 418 439 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 440 460 4 (POTENTIAL).
 FT DOMAIN 461 483 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 484 504 5 (POTENTIAL).
 FT DOMAIN 505 532 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 533 553 6 (POTENTIAL).
 FT DOMAIN 554 584 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 585 605 7 (POTENTIAL).
 FT DOMAIN 605 694 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 30 151 FZ.
 FT DOMAIN 168 172 POLY-PRO.
 FT TRANSMEM 194 202 POLY-GLY.
 FT DOMAIN 211 216 POLY-GLY.
 FT DOMAIN 639 663 POLY-GLY.
 FT SITE 608 613 LYS-THR-X-X-TRP MOTIF.
 FT SITE 692 694 PDZ-BINDING.
 FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 694 AA; 73300 MW; E740CBFDA2A233EF CRC64;

Query Match 62.9%; Score 824; DB 1; Length 694;
 Best Local Similarity 59.9%; Pred. No. 2.1e-57;
 Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;

Oy 11 SILL-LILLALQVGRAAAASKAPVQCOITVPMCRGIGYNLTHMPNQFNHDDEAGLEVH 68
 Db 11 SILLALLQVGRAAAASKAPVQCOITVPMCRGIGYNLTHMPNQFNHDDEAGLEVH 70

QY 69 QFWPLVEIQCSPDRLPFLCTMTPCLPDYKPLPPCRSYCERAKAGCSPLMRQYGFAMP 128
 CC :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
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 CC or send an email to license@ibab-sib.ch).
 CC
 DR EMBL; U4321; ANC52433.1; -.
 DR MGD; MGI; I08460; Fzdb.
 DR InterPro; IPR00539; Frizzled.
 DR InterPro; IPR00024; Fz_domain.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF01534; Frizzled; 1.
 DR PRINTS; PR00483; FRIZZLED.
 DR SMART; SM0063; FRI; 1.
 DR PROSITE; PSS0038; Fz; 1.
 DR PROSITE; PS50201; G PROTEIN RECEPTOR F2-4; 1.
 KW Multi-gene family; G-protein-coupled receptor; Transmembrane;
 KW Developmental protein; Glycoprotein; Signal.
 PT SIGNAL 1
 PT
 FZDB_MOUSE STANDARD; PRT; 685 AA.
 ID FZDB_MOUSE
 AC 06109;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled B precursor (Frizzled-8) (Fz-8) (mFz8).
 GN FZDB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N A.
 RX MEDLINE=96224032; PubMed=8626600;
 RA Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P.,
 RA Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;
 RT "A large family of putative transmembrane receptors homologous to the
 RT product of the Drosophila tissue polarity gene frizzled.";
 RL J. Biol. Chem. 271:4476-4476(1996).
 RN [2]
 RP COUPLING TO BETA-CATENIN PATHWAY.
 RX MEDLINE=93032425; PubMed=1039542;
 RA Sheldahl L.C., Park M., Malbon C.C., Moon R.T.;
 RT "Protein kinase C is differentially stimulated by Wnt and Frizzled
 RT protein in a G-protein-dependent manner.";
 RL Cur. Biol. 9:685-688(1999).

-1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 are coupled to the beta-catenin canonical signaling pathway, which
 leads to the activation of dishevelled proteins, inhibition of
 GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 of Wnt target genes. A second signaling pathway involving PKC and
 calcium fluxes has been seen for some family members, but it is
 not yet clear if it represents a distinct pathway or if it can be
 integrated in the canonical pathway, as PKC seems to be required
 for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 to involve interactions with G-proteins. May be involved in
 transduction and intercellular transmission of polarity
 information during tissue morphogenesis and/or in differentiated
 tissues. Activation by Wnt8 induces expression of beta-catenin
 target genes.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- TISSUE SPECIFICITY: Expressed in chondrocytes.

-1- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of
 the Wnt/beta-catenin signaling pathway (By similarity)

-1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 similarity).

-1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 RECEPORS.

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 CC or send an email to license@ibab-sib.ch).
 CC
 DR EMBL; U4321; ANC52433.1; -.
 DR MGD; MGI; I08460; Fzdb.
 DR InterPro; IPR00539; Frizzled.
 DR InterPro; IPR00024; Fz_domain.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF01534; Frizzled; 1.
 DR PRINTS; PR00483; FRIZZLED.
 DR SMART; SM0063; FRI; 1.
 DR PROSITE; PSS0038; Fz; 1.
 DR PROSITE; PS50201; G PROTEIN RECEPTOR F2-4; 1.
 KW Multi-gene family; G-protein-coupled receptor; Transmembrane;
 KW Developmental protein; Glycoprotein; Signal.
 PT SIGNAL 1
 PT
 FZDB_MOUSE STANDARD; PRT; 685 AA.
 ID FZDB_MOUSE
 AC 06109;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled B precursor (Frizzled-8) (Fz-8) (mFz8).
 GN FZDB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N A.
 RX MEDLINE=96224032; PubMed=8626600;
 RA Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P.,
 RA Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;
 RT "A large family of putative transmembrane receptors homologous to the
 RT product of the Drosophila tissue polarity gene frizzled.";
 RL J. Biol. Chem. 271:4476-4476(1996).
 RN [2]
 RP COUPLING TO BETA-CATENIN PATHWAY.
 RX MEDLINE=93032425; PubMed=1039542;
 RA Sheldahl L.C., Park M., Malbon C.C., Moon R.T.;
 RT "Protein kinase C is differentially stimulated by Wnt and Frizzled
 RT protein in a G-protein-dependent manner.";
 RL Cur. Biol. 9:685-688(1999).

Query Match 62.9%; Score 823 5; DB 1; Length 685;
 Best Local Similarity 60.0%; Pred. No. 2.3e-57;
 Matches 159; Conservative 24; Mismatches 39; Index 43; Gaps 8;

QY 11 SLL-LLLAQVGRAAASKAPVQEITPMPGRCIGLYNLTMMQNFMHDTDAGLEVH 68
 CC :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 CC 11 SLLAAALAVIQLRSGGAAAKELAQEITWPLKGIGVNTYMQNFMDTDAGLEVH 70
 CC
 DR 71 QFWPLVEIQCSPDRLPFLCTMTPCLPDYKPLPPCRSYCERAKAGCSPLMRQYGFAMP 128
 DR 71 QFWPLVEIQCSPDRLPFLCTMTPCLPDYKPLPPCRSYCERAKAGCSPLMRQYGFAMP 130
 DR 131 DRMRCDRLPQQ-NFDLCLMDYNSEATA--PPRPFPAKPTLPG-----PPG 188
 DR 175 A-----PASGCGC-PAGGPV---CKCREPFVPIKESHLINK 209
 DR 189 ARPPHRGGSSRGSDAAAAPPSSRGKARPPGGAAACPGCQCRAPMVSVSERHLYNR 248
 QY 210 VRTGQVNPNCAPVCPICQPSFSADETRF 234
 DB 249 WKTGQIANCALPCINPPFSQDERAF 273

RESULT 6

ID FZDB_XENLA STANDARD; PRT; 581 AA.

AC 093274; Q9Y155;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Frizzled 8 precursor (Frizzled-8) (Fz-8) (Xfz8).
GN FZ8.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bureleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopidae; Xenopus.
OX NCBI_TAXID=8355;
RN [1]
RP SEQUENCE FROM N.A., AND COUPLING TO BETA-CATENIN PATHWAY.
RC TISSUE=Embryo;
RX MEDLINE=98301424; PubMed=9636083;
RA Deardrif M.A., Tan C., Conrad L.J., Klein P.S.;
RT "Frizzled-8 is expressed in dorsal development.";
RL Mech. Dev. 74:145-157(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=98301424; PubMed=9636083;
RA Deardrif M.A., Tan C., Conrad L.J., Klein P.S.;
RT "Frizzled-8 is expressed in the Spemann organizer and plays a role in
early morphogenesis.";
RL Development 125:2667-2700(1998).
CC -!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
are coupled to the beta-catenin canonical signaling pathway, which
leads to the activation of dishevelled proteins, inhibition of
GSK-3 kinase, nuclear accumulation of beta-catenin and activation
of Wnt target genes. A second signaling pathway involving PKC and
calcium fluxes has been seen for some family members, but it is
not yet clear if it represents a distinct pathway or if it can be
integrated in the canonical pathway as PKC seems to be required
for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
to involve interactions with G-Proteins. May be involved in
transduction and intercellular transmission of polarity
information during tissue morphogenesis and/or in differentiated
tissues. Activation by Wnt8, Wnt5A or Wnt3A induces expression of
beta-catenin target genes. Displays an axis-inducing activity.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- DEVELOPMENTAL STAGE: First expressed at high levels in the late
blastula stages. At early gastrula, expressed in the deep cells of
the Spemann organizer prior to involution of the dorsal blastopore
lip. Detected in presumptive neuroectoderm as gastrulation
proceeds. Becomes restricted to the anterior ectoderm by the end
of gastrulation. At neurula stages, localized in the most anterior
region of the embryo, mainly in the anterior ectoderm including
telencephalic and cement gland regions.
-!- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of
the Wnt/beta-catenin signaling pathway (By similarity).
-!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
similarity).
-!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (Fz) DOMAIN.

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the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50261; G PROTEIN RECEP F2_4; 1.
KW Multigene family; G-protein-coupled receptor; Transmembrane;
KW Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 581 FRIZZLED B.
FT DOMAIN 24 239 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 240 260 1 (POTENTIAL).
FT DOMAIN 261 271 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 272 292 2 (POTENTIAL).
FT DOMAIN 293 320 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 321 341 FRIZZLED B.
FT DOMAIN 342 377 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 378 398 4 (POTENTIAL).
FT DOMAIN 399 407 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 408 428 5 (POTENTIAL).
FT DOMAIN 429 454 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 455 475 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 476 505 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 506 526 7 (POTENTIAL).
FT DOMAIN 527 581 FZ.
FT DOMAIN 524 144 LYS-THR-X-X-X-TRP MOTIF.
FT SITE 529 534 PDZ-BINDING.
FT SITE 579 581 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 MES --> MECPY (IN REF. 2).
FT CONFLICT 1 3 S --> L (IN REF. 2).
FT CONFLICT 7 7 L --> V (IN REF. 2).
FT CONFLICT 10 10 W --> G (IN REF. 2).
FT CONFLICT 14 14 C --> S (IN REF. 2).
FT CONFLICT 20 20 G --> S (IN REF. 2).
FT CONFLICT 135 135 G --> S (IN REF. 2).
FT CONFLICT 171 171 G --> A (IN REF. 2).
FT CONFLICT 175 175 V --> A (IN REF. 2).
FT CONFLICT 185 185 T --> P (IN REF. 2).
FT CONFLICT 216 216 I --> T (IN REF. 2).
FT CONFLICT 237 237 E --> D (IN REF. 2).
FT CONFLICT 494 496 PEM --> SEG (IN REF. 2).
FT CONFLICT 500 500 H --> R (IN REF. 2).
FT CONFLICT 547 547 A --> T (IN REF. 2).
FT CONFLICT 565 565 G --> A (IN REF. 2).
FT CONFLICT 572 572 C --> Y (IN REF. 2).
FT CONFLICT 572 581 AA; 65378 MW; 8089CC408AB21E23 CRC64;
SQ SEQUENCE

Query Match Score 802; DB 1; Length 581;
Best Local Similarity 63.9%; Pred. No. 9.5e-56;
Matches 149; Conservative 25; Mismatches 43; Indels 16; Gaps 5;

Qy 13 LILLIAOLQVGRAAASKAPVQEQITWPMCRGGIGNLTHMNPQHNDTQEAGLEHQFWMP 72
Db 8 LILLIVSWLQLGSQCAAKELSCQELITVPLCKDIGNYNTYMPNQHNDTQEAGMEVHQFWP 67

Qy 73 LVEIQOSPDLRFLCTWYTPICLDPYHKPFCRSVCRERAKAGESPLMROGYGAPEWMS 132
Db 68 IIVVHICPSDPUKFLGSMWTCILEYKKPLPCRSVCRERAKAGESPLMROGYGAPEWMS 127

Qy 133 CDRLPVIGRDVLCMD-YNRSEAT-APPRLPKP-----TLRQPGPAGASGE 181
Db 128 CDRLPVQG-NPDILCMDYNRSEATTAAPSPKEPPKPPPARSVPKRTRVPPRSRSRATG 186

Qy 182 CPAGGPFLVCKCREPVYILKESHPLYNKVRTGQVNCAVCPYQPSFSADERTF 234
Db 187 CESG----CQCRAPMVQVSNERHPLNVRGQIPNCAMPCHNPFPSBRTF 235

RESULT 7

ID_FZ2_DROME STANDARD; PRT; 694 AA.
AC Q9VVK3; Q9y156; 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DR PRINTS; PRO0489; FRIZZLED.

DE Frizzled protein 2 precursor (Frizzled-2) (DFz2).
 GN FZ2 OR CG9739.
 OS Drosophila melanogaster (Fruit fly).
 OC
 Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydioidea; Drosophilidae; Drosophila.
 OC NCBI_TAXID=7227;
 RN [1] SEQUENCE FROM N.A., AND BINDING TO WINGLESS THROUGH FZ DOMAIN.
 RX MEDLINE=96553971; PubMed=8717056;
 RA Bhanot P., Brink M., Samos C.H., Hsieh J.C., Wang Y., Macke J.P.,
 Andrew D., Nathans J., Nusse R.;
 RT "A new member of the frizzled family from *Drosophila* functions as a
 Wingless receptor.";
 RL Nature 382:225-230 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Berkley;
 MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scheier S.E., Li P.W., Hoskins R.A., Galle R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazquez R.G., Champe M., Preiff B.D.,
 Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 Abil J.F., Agbyanii A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borkova D., Butchan M.R., Bouck J., Brokstein P., Brottier P.,
 Burtis K.C., Busam D.A., Butler H., Cadie E., Centner A., Chandra I.,
 Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablo B., Dalcier A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 Fosler C., Gabriel A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 Lasko P., Lei Y., Levittky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPhereson D.,
 Merkulov G., Mishina N.V., Moarry C., Morris J., Mosheff A.,
 Mount S.M., Moy M., Murphy L., Muzy D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Pacieb J.J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reeve M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier B., Spradling A.C., Stapleton M., Strong R., Sun B.,
 Svistek R., Tector C., Turner C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).
 CC -!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 are coupled to the activation of dishevelled proteins, inhibition of
 leads to the activation of betacatenin and activation
 of Wnt target genes. A second signalling pathway involving PKC and
 calcium fluxes has been seen for some family members, but it is
 not yet clear if it represents a distinct pathway or if it can be
 integrated into the canonical pathway, as PKC seems to be required
 for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 to involve interactions with G-proteins. Required to coordinate
 the cytoskeletons of epidermal cells to produce a parallel array
 of cuticular hairs and bristles.
 -!- SUBCELLULAR LOCATION: Integral membrane protein (potential);
 -!- SUBCELLULAR LOCATION: Expression starts at stage 6 in all cells
 between 15 and 70 per cent of egg length, including the
 invaginating cells of the ventral furrow. Stripe pattern is

CC emerging by early stage 8. From stage 9 and continuing throughout
 embryogenesis, expression is seen in the developing CNS. At stage
 10, expressed in 15 stripes in the presumptive head and trunk
 regions, in the posterior midgut primordium, in a subset of cells
 of anterior midgut invagination and in the procephalic lobe. At
 stage 12, expression declines in epidermis and increases in the
 midgut and visceral mesoderm. At stage 17, only expressed in the
 CNS, hindgut, and dorsal vessel.
 CC CNS, hindgut, and dorsal vessel.
 CC -!- DOMAIN: LYB-Thr-X-X-Trp motif is involved in the activation of
 the Wnt/beta-catenin signaling pathway (By similarity).
 CC -!- DOMAIN: The fz domain is involved in binding with Wnt ligands.
 CC -!- SIMILARITY: BELONGS TO FAMILY FZ/SMO Of G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
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 or send an email to license@isb-sib.ch).
 CC DR EMBL; AE003518; AAC47273.1; -.
 CC DR FlyBase; FBgn0016797; Fz2.
 CC DR InterPro; IPR000539; Frizzled.
 CC DR InterPro; IPR000024; Fz domain.
 CC DR InterPro; IPR000832; GPC_R Secretin.
 CC DR Pfam; PF01534; Frizzled; T.
 CC DR Pfam; PF01392; Fz; 1.
 CC DR PRINTS; PRO0489; FRIZZLED.
 CC DR SMART; SM00063; FRI; 1.
 CC DR PROSITE; PSS0018; Fz; 1.
 CC DR PROSITE; PSS0261; G-PROTEIN RECEP_P2_4; 1.
 CC DR MULTIGE Family; Receptor; G-protein coupled receptor; Transmembrane;
 KW Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1 22
 FT POTENTIAL 1 22
 FT CHAIN 23 694
 FT FRIZZLED PROTEIN 2.
 FT DOMAIN 23 315
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 316 336
 FT 1 (POTENTIAL)
 FT DOMAIN 337 352
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 353 373
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 374 397
 FT TRANSMEM 398 418
 FT DOMAIN 419 439
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 440 460
 FT 4 (POTENTIAL)
 FT DOMAIN 461 482
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 483 503
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 504 534
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 535 555
 FT DOMAIN 556 584
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 585 605
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 606 694
 FT GLY-RICH.
 FT DOMAIN 187 225
 FT FZ.
 FT LYS-THR-X-X-TRP MOTIF.
 FT SITE 59 180
 FT 608 613
 FT PDZ-BINDING.
 FT CARBOHYD 692 694
 FT N-LINKED (GlcNAc. . .) (POTENTIAL).
 FT CARBOHYD 698 708
 FT N-LINKED (GlcNAc. . .) (POTENTIAL).
 FT CONFLICT 55 55
 FT V -> A (IN REF. 1).
 FT CONFLICT 417 417
 FT S -> T (IN REF. 1).
 SQ 694 RA 75451 MW 6C510P13CBABF096 CRC64;

Query Match 47.4%; Score 621; DB 1; Length 694;
 Best Local Similarity 43.4%; Pred. No. 1.6e-41; Gaps 7;
 Matches 124; Conservative 27; Mismatches 55; Index 80;
 Oy 22 GRAAASKAP-----VQOBITWMCRGTYGNYTHMPNQFNHDQDEAGLEVH 68
 Db 40 GHGLDASPAFGVGVPVKPPNRCEBTFMCRGIGYNTSPFNEMNHBTDAGLEVH 99

Qy 225 PS-----FSADERTPA 235
 ID : FZD2_MOUSE STANDARD; PRT; 570 AA.
 AC Q9JIP6; Q9U1PS; Q9WUJ2;
 DR 227 PARPGSMFSSQEETRFA 244
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DB prizelized 2 precursor (Frizzled-2) (Fz-2) (mFz2) (mFz10).
 GN FZD2 OR FZD10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus; NCBI_Taxid=10090;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Fetal gut;
 RX MEDLINE=20136324; PubMed=10903145;
 RA Malik T.H., Shivedasani R.A.;
 RT "Structure and expression of a novel frizzled gene isolated from the mouse model of prostate cancer";
 RL Biochem. J. 349:829-834 (2000).
 RN [2] SEQUENCE OF 172-312 FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Prostate;
 RA Johnson M.A., Greenberg N.M.;
 RT "Characterization of the wnt signaling cascade in the TRAMP transgenic mouse model of prostate cancer";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Receptor for wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as FRC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in embryonic and adult heart, lung, chondrocytes and brain. Also expressed in the developing gastrointestinal tract (strongest in foregut), much weaker expression in the adult. No expression in fetal liver and adult spleen. Up-regulated in oesophageal squamous cell carcinomas.
 CC -!- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the wnt/beta-catenin signalling pathway (By similarity).
 CC -!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).
 CC -!- SIMILARITY: BELONGS TO FAMILY RZ/SMO OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
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 CC EMBL; AF206321; AAF74056.1; -;
 DR AF206322; AAF74057.1; -;
 DR EMBL; AF119183; AAD8286.1; -;
 DR MGD; MGI:1888513; FZD2.
 DR RESULT 9
 DR FZD2_MOUSE STANDARD; PRT; 570 AA.
 DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR000024; Fz_domain.
 DR InterPro; IPR000832; GPCR_Secretin.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF01534; Frizzled; 3.
 DR PRINTS; PRO0489; FRIZZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS50038; FZ; 1.
 DR PROSITE; PS50201; G_PROTEIN_RECEP_F2_4; 1.
 KW Multigene family; G-protein-coupled receptor; Transmembrane; Developmental Protein; Glycoprotein; Signal.
 FT SIGNAL 1 28 POTENTIAL.
 FT CHAIN 29 570 FRIZZLED 2.
 FT DOMAIN 29 252 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 253 273 1 (POTENTIAL).
 FT DOMAIN 274 284 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 285 305 2 (POTENTIAL).
 FT DOMAIN 306 332 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 333 353 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 354 375 3 (POTENTIAL).
 FT TRANSEM 376 396 4 (POTENTIAL).
 FT DOMAIN 397 419 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 420 440 5 (POTENTIAL).
 FT DOMAIN 441 466 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 467 487 6 (POTENTIAL).
 FT DOMAIN 488 524 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 525 545 7 (POTENTIAL).
 FT DOMAIN 546 570 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 570 592 PZ.
 FT SITE 548 553 POLY-GLY.
 FT SITE 568 570 LYS-THR-X-X-X-TRP MOTIF.
 FT CARBOHYD 58 58 PDZ-BINDING.
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 307 307 E -> K (IN REF. 2).
 FT SEQUENCE 570 AA; 64058 MW; 798577F7D10FC51A CRC64;
 DR Query Match 36.3%; Score 476; DB 1; Length 570;
 DR Best Local Similarity 41.5%; Pred. No. 2.9e-30;
 DR Matches 107; Conservative 31; Mismatches 82; Indels 38; Gaps 10;
 DR Sequence 6 ALPRDSLAPPSSILLILQLVGRAAASKAPV-----COITVPMCRGIGYNLTHMPNQ 54
 DR 6 ALPRDSLAPPSSILLILQLVGRAAASKAPV-----COITVPMCRGIGYNLTHMPNQ 54
 DR 55 FNHDIDDEAGIEVSHOFWPLVTEIQSPDLPFLCTMYTPCLPDHKPLPERSYERAKA 114
 DR 66 LIGHTBODAGLEVHOPYPLVKQWPSPLERLFCMNVAPCVTV-LBQATIPCRSICERAO 124
 DR 115 GCSPLMRQYGFPAWPERMSCORPLVGRDAELVLMYNRSE----ATTAPRPPPKPT 168
 DR 125 GCEALUNKNGFRQWPERLCRHFPRHG--AEQICVGONHSEBDGAPALLTAPPGLU-QPG 180
 DR 169 ILPQQPAGAPSGGECAGG---PVVCKCIBPFVPLKESHPLYNKVRQVNPNCAVPCYQ 224
 DR 181 AGGTGPGGGGGSPRYATHEHPFHCP----RVLKV--PSYLSYKFLGERDCAPC-E 231
 DR 225 PS-----FSADERTPA 235
 DR 232 PARPGSMFSSQEETRFA 249
 DR RESULT 10
 DR FZD2_RAT STANDARD; PRT; 570 AA.
 DR FZD2_RAT STANDARD; PRT; 570 AA.
 DR 008474; Frizzled; 3.
 DR 15-JUN-2002 (Rel. 41, Last sequence update)
 DR 15-JUN-2002 (Rel. 41, Last annotation update)
 DR Frizzled 2 precursor (Frizzled-2) (rFz2).
 DR FZD2.
 OS Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Osteosarcoma;
 RX Chan S.D.H., Karpf D.B., Fowlkes M.E., Hooks M., Bradley M.S.,
 RA Vuong V., Bambino T., Liu M.Y.C., Arnaud C.D., Strewler G.J.,
 RA Nissenbaum R.A.;
 RT "Two homologs of the Drosophila polarity gene frizzled (fz) are widely
 expressed in mammalian tissues.";
 RT J. Biol. Chem. 267:2202-25207(1992).
 RL RN [2]
 RP WNT-MEDIATED PKC ACTIVATION.
 RX MEDLINE=99324245; PubMed=0395542;
 RA Sheldahl L.C., Park M., Malbon C.C., Moon R.T.;
 RT "Protein kinase C is differentially stimulated by Wnt and Frizzled
 homologs in a G-protein-dependent manner.";
 Curr. Biol. 9:655-658(1999).
 !- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 are coupled to the beta-catenin canonical signaling pathway, which
 leads to the activation of dishevelled proteins, inhibition of
 GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 of Wnt target genes. A second signaling pathway involving PKC and
 calcium fluxes has been seen for some family members, but it is
 not yet clear if it represents a distinct pathway or if it can be
 integrated in the canonical pathway, as PKC seems to be required
 for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 to involve interactions with G-proteins. May be involved in
 transduction and intercellular transmission of polarity
 information during tissue morphogenesis and/or in differentiated
 tissues. Activation by Wnt5A stimulates PKC activity via a G-
 protein-dependent mechanism.
 !- SUBCELLULAR LOCATION: Integral membrane protein.
 !- TISSUE SPECIFICITY: Widely expressed. Most abundant in kidney,
 liver, uterus, ovary and heart. Lower levels
 at intestinal. Extremely low in calvaria, mammary glands and testis.
 !- DEVELOPMENTAL STAGE: Expressed predominantly in neonatal tissues,
 at lower levels in adult.
 !- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of
 the Wnt/beta-catenin signalling pathway (By similarity).
 CC -!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 similarity).
 CC -!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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 or send an email to license@isb-sib.ch).

RESULT 11
 FZD7_HUMAN
 ID FZD7_HUMAN - STANDARD; PRT; 574 AA.
 AC O75084; O94816; 1
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DR 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled 7 precursor (Frizzled-7) (FZD7) (FZE3).
 GN FZD7.
 OS Homo sapiens (Human).
 OC Bokaryota; Metacoda; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND COUPLING TO BETA-CATENIN PATHWAY.
 RC TISSUE-Oesophageal carcinoma;
 RX MEDLINE=98374322; PubMed=9770118;
 RA Tanaka S., Akiroshi T., Mori M., Wands J.R., Sugimachi K.;
 RT "A novel frizzled gene identified in human esophageal carcinoma
 mediates APC/beta-catenin signals";
 RT Proc. Natl. Acad. Sci. U.S.A. 95:10164-10169(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal lung;
 RX MEDLINE=99032814; PubMed=9813155;
 RA Sagara N., Toda G., Hirai M., Terada M., Katoh M.;
 RT "Molecular cloning, differential expression, and chromosomal
 localization of human frizzled-1, frizzled-2, and frizzled-7.";
 RT Biochem. Biophys. Res. Commun. 252:117-122(1998).

CC -!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: High expression in adult skeletal muscle and fetal kidney, followed by fetal lung, adult heart, brain, and placenta. Specifically expressed in squamous cell esophageal carcinomas.

CC -!- DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity). The fz domain is involved in binding with Wnt ligands (By similarity).

CC -!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.

CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (Fz) DOMAIN.

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CC EMBL: AB010881; BAA32424 1; -.

DR EMBL; AB017365; BAA34668 1; -.

DR Genew; HGNC; 4005; FZD7.

DR MIM: 603420; -.

DR InterPro; IPR000539; Frizzled.

DR InterPro; IPR000024; Fz domain.

DR InterPro; IPR000832; GPCR_secretin.

DR Pfam; PF01392; Fz; 1.

DR Pfam; PF01534; Frizzled; 1.

DR SMART; SMC0063; FRI_1.

DR PROSITE; PS50038; FZ; 1.

DR PROSITE; PS50061; G-PROTEIN_RCCEP_F2_4; 1.

KW Multi-Gene Family; G-protein_coupled_receptor; Transmembrane; Developmental protein; Glycoprotein; Signal.

PT SIGNAL 1

PT CHAIN 33

PT DOMAIN 33

PT TRANSMEM 256

PT DOMAIN 277

PT TRANSMEM 278

PT DOMAIN 289

PT TRANSMEM 310

PT DOMAIN 336

PT TRANSMEM 337

PT DOMAIN 358

PT TRANSMEM 379

PT DOMAIN 390

PT TRANSMEM 401

PT DOMAIN 424

PT DOMAIN 445

PT TRANSMEM 471

PT DOMAIN 492

PT TRANSMEM 529

PT DOMAIN 550

PT DOMAIN 44

PT DOMAIN 445

PT TRANSMEM 471

PT SITE 572

PT CARBOHYD 63

PT CARBOHYD 164

PT CONFLICT 8

CC 552

CC 557

CC 574

CC 63

CC 164

CC 8

CC 15

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	RESULT 12	
ID	FZD7_MOUSE	STANDARD;
AC	061050	PRT;
DT	15-JUN-2002 (Rel. 41, Created)	
DT	15-JUN-2002 (Rel. 41, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Frizzled 7 precursor (Frizzled-7) (Fz-7) (m7z7).	
GN	FZD7.	
OS	Mus musculus (Mouse)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10930;	
RN	[1]-	
RP	SEQUENCE FROM N. A.	
RX	MEDLINE=96224032; PubMed=8626800;	
RA	Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;	
RT	"A large family of putative transmembrane receptors homologous to the product of the Drosophila tissue polarity gene frizzled.";	
RL	J. Biol. Chem. 271:4468-4476(1996).	
RN	[2]	
RP	COPPLING TO BETA-CATENIN PATHWAY.	
RX	MEDLINE=9324245; PubMed=10395542;	
RA	Sheldahl L.C., Park M., Malbon C.C., Moon R.T.;	
RT	"Protein kinase C is differentially stimulated by Wnt and Frizzled homologs in a G-protein-dependent manner.";	
RL	Curr. Biol. 9:695-698(1999).	
CC -!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity		

CC or send an email to license@ibz-sib.ch).

RN [1] SEQUENCE FROM N.A.

RC TISSUE: limb bud;

RC MEDLINE=98260739; PubMed=9598377;

RA Kangaku M., Twombly V., Tabin C.;

RT "Expression of wnt and frizzled genes during chick limb bud development";

RT Cold Spring Harb. Symp. Quant. Biol. 62:421-429(1997).

RN [2] SEQUENCE OF 307-592 FROM N.A.

RP MEDLINE=20245319; PubMed=10781956;

RA Stark M.R., Biggs J.J., Schoenwolf G.C., Rao M.S.;

RT "Characterization of avian frizzled genes in cranial placode development";

RT Mech. Dev. 93:195-200(2000).

RL Mech. Dev. 93:195-200(2000).

CC -!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled protein, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. -!- TISSUE SPECIFICITY: Expressed in the lens, otic placode (medial wall of the vesicle) and in epibranchial placode. Also expressed in the developing somites (dermomyotome).

CC -!- DEVELOPMENTAL STAGE: Somites and placodal expression appears at stage 9. At this stage, more obvious expression is detected in the neural tube (midbrain and rostral hindbrain), and persists through about stage 15. Strongly expressed in the ectoderm and around the optic placodes at stage 12. At stage 16, otic expression declines, expression in epibranchial placodes begins and peaks at stage 20. Expression in the lens of the eye is first seen at about stage 15, more evident at stage 16. At stage 17, seen in the ectoderm and mesenchyme of the limb primordia. Detected at stage 20 in the lip of the optic cup, in the mesenchyme surrounding the eye. In the ectoderm overlying the lens and in the ectoderm caudal and ventral of the olfactory placodes. From stages 20-30, expressed in cartilage and in the dermomyotomes and migrating sclerotomal cells forming vertebrae.

CC -!- DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).

CC -!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).

CC -!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.

CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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CC EMBL; AF139165; AAF065959.1; -.

DR EMBL; AF24314; AAF61094.1; -.

DR InterPro; IPR00539; Frizzled.

DR InterPro; IPR00024; Fz domain.

DR InterPro; IPR00832; GPCR_Secretin.

DR Fzam; PF01192; Fz; 1.

DR Fzam; PF01134; Frizzled; 2.

DR PRINTS; PRO0489; FRIZZLED.

DR SMART; SM0063; FRI; 1.

DR PROSITE; PS50038; FZ; 1.

DR PROSITE; PS50261; G PROTEIN RECEP F2 4; 1.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus gallus (Chicken).

NCBI TaxID:9031;

FT CONFLICT 352 352 S -> F (IN REF. 2).
 SQ SEQUENCE 642 AA; 70955 MW; 0AADC0DC820B6CE CRC64;
 Query Match 32.2%; Score 422; DB 1; Length 642;
 Best Local Similarity 36.0%; Pred. No. 5.4e-26;
 Matches 102; Conservative 32; Mismatches 87; Indels 62; Gaps 10;
 Qy 3 RPDPSAPPULLL-----AQVGRAAA-ASKAP----- 31
 Db 44 RADPRRWAQGLLWLLEAPLLGSGVRAQAGQVSGPGQAPPPQQPQQSGQQVNGERGI 103
 Qy 32 -----VCQEITVPMCGIGIGNLTIMPQFHDTDDEAGLEVHQIWPLVETQCS3DLRFF 85
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Qy 86 LCTMMPYPICLDYHKQLUPCRSVCRAKACSPRLRQYGRPWMSCDLUPVUQGRDAEV 145
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 164 LCSMAPVCTV-LEQKLUPPERSICERARQGEALMKFGTQWPTDIKEPKPVHG---AGE 220
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Qy 146 LCMDNKRSEATTAPPFPKPLTQPPGAPASGCCPAG----GPFVCKCRRPFVPI 199
 |||||:|||||:|||||:|||||:|||||:|||||:
 Db 221 LCVGGQNTSDKGTPTRSLPWFWSKQHGGGGYRGCGYPGGAGTVRKGKESCP-RAILVPS 279
 |||||:|||||:|||||:
 Qy 200 LKESHLINKRTGQVNCAVPCYGS-----PSADERIFA 235
 |||||:|||||:
 Db 280 YLNVHRLGEK-----DCGAPC-BPTKVIGLMYFPEELRFS 314
 |||||:|||||:
 Search completed: May 19, 2003, 16:34:31
 Job time : 16 SECs



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Om protein - protein search, using sw model

Run on: May 19, 2003, 16:33:07 ; Search time 33 Seconds
 (without alignments)
 1467.305 Million cell updates/sec

Title: Perfect score: US-09-847-102A-68

Sequence: 1 MARPPSAPSSULLLQL.....PNCANVPCYQFSPRSADERTFA 235

Scoring table: BUCSUMG2 Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTREMBL 21;*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_uniclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	801	61.1	579	13 Q9Y100	Q9y100 brachydanio
2	801	61.1	579	13 Q9W6B4	Q9w6e4 brachydanio
3	800	579	13 Q9PTT7	Q9ptt7 brachydanio	
4	796	60.8	592	13 Q9WB22	Q9we22 brachydanio
5	794	60.6	576	13 Q9Y149	Q9y149 brachydanio
6	794	60.6	576	13 Q9PK65	Q9pk6 brachydanio
7	794	60.6	576	13 Q9PMW8	Q9pmw8 brachydanio
8	461	35.2	574	4 Q96B74	Q96b74 homo sapien
9	451	34.4	550	5 Q9UB06	Q9ub06 caenorhabdi
10	429.5	32.8	550	13 Q901I7	Q9y017 brachydanio
11	426	32.5	872	5 Q9N145	Ogn145 clona intest
12	410.5	31.3	559	13 Q902T3	Q902t3 brachydanio
13	408.5	31.2	559	13 Q9BS12	Q9bs12 brachydanio
14	403	30.8	557	13 Q8QFM3	Q8qfm3 brachydanio
15	401.5	30.6	591	4 Q8TANZ	Q8tan2 homo sapien
16	380.5	29.0	577	13 Q918V7	Q9y18v7 brachydanio

SEQUENCE FROM N.A.
 RP
 RC STRAIN=ORGCON;
 RX MEDLINE=93077702; PubMed=9858730;
 RA Kim S.H., Park H.C., Yeo S.Y., Hong S.K., Choi J.W., Kim C.H.,
 RA Weinstein B.M., Huh T.L.,
 "Characterization of two frizzled8 homologues expressed in the embryonic shield and prechordal plate of zebrafish embryos.",
 RT Mech. Dev. 78:193-201(1998).
 RT EMBL; AF00697; AADD5435.1; -.
 DR ZFIN; ZDB-GENE:000328-3; fz8a.
 DR InterPro; IPR00539; Frizzled.
 DR InterPro; IPR00024; Fz Domain.
 DR Inter-Pro; IPR000832; GPCR secretin.
 DR Pfam; PF0534; Frizzled; T.
 DR Pfam; PF01392; Fz; 1.
 DR PRINTS; PR00489; FRIZZLED.
 DR SMART; SM0063; FRI_1.
 DR PROSITE; PS50261; G-PROTEIN RECEPTOR_F2_4; 1.
 DR PROSITE; PS50268; G-PROTEIN RECEPTOR_F2_4; 1.
 SQ SEQUENCE 579 AA; -65249 MW; AF5AC9C626A4EC06 CRC64;

Query Match 61.1%; Score 801; DB 13; Length 579;
 Best Local Similarity 63.1%; Pred. No. 36-69; Indels 16; Gaps 6;
 Matches 147; Conservative 25; Mismatches 45;

DR PFam; PF01392; Fz; 1.
 DR PRINTS; PR00489; FRIZZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS50038; FZ; 1.
 DR SEQUENCE; PSS061; G_PROTEIN_RECER_F2_4; 1.
 Best Local Similarity 60.8%; Score 796; DB 13; Length 592;
 Matches 152; Conservative 67.9%; Pred. No. 9; 3e-69; Mismatches 51; Indels 4; Gaps 4;

Qy 12 LLLULILQLVGRAAAASKAPVCQETVPMERGIGGNLTMPNQFNHDTOEAGLEHQFW 71
 24 LHVLUFOLSLGDSASKDIVEPPTVPMKGIGNTYMPNQFNHDTOEAGLEHQFW 83

Db 72 PLVEIQCSPDLRFFLCTMYTPICLDPYHKPLPCCSVCEAKAGKAGSPLMRYQGRWPERM 131
 84 PLVRHCSPPDLFLFGSMYTPICLDPYKKPLPCCSVCEAKAGKAGSPLMRYQGRWPERM 143

Qy 132 SCDRLVPLGRDAEVLMYDYNRSEATTAPPRPFPAKTLPGPPGAPASGGCPAGG-PFVC 190
 144 SCEOQMLG-DTDRCLDRNSETTTLSP-PFP-KTPKGTPRHRATKSAPPQCCDREC 200

Db 191 KCREPPVPIKESHLINKRTGQFNCAPCVCYQPSFSADERTF 234
 201 HCRGPVLVPVIKEAHPLHNRYNTGSLPNCAALPCHQPFQSQDBRTF 244

RESULT 5
 QYIY19 PRELIMINARY; PRT; 576 AA.
 ID QYIY19; AC 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DB 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 GN Fz2B.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1];
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON;
 RX MEDLINE=9077702; PubMed=9858730;
 RA Kim S.H., Park H.C., Yeo S.Y., Hong S.K., Choi J.W., Kim C.H.,
 Weintraub B.M., Huh T.L.;
 RT "Characterization of two frizzled8 homologues expressed in the
 embryonic shield and prechordal plate of zebrafish embryos.";
 RL Mech. Dev. 78:193-198 (1998).
 DR EMBL; AF060695; AAC117520; 1; -.
 DR ZFIN; ZDB-GENE-000328-4; Fz8B.
 DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR00024; Fz domain.
 DR InterPro; IPR00032; GPCR_Secretin.
 DR Pfam; PF01534; Frizzled; 1.
 DR PRINTS; PR00489; FRIZZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS50038; FZ; 1.
 DR PROSITE; PS50061; G_PROTEIN_RECER_F2_4; 1.
 DR SEQUENCE; PSS061; G_PROTEIN_RECER_F2_4; 1.

Query Match 60.6%; Score 794; DB 13; Length 576;
 Best Local Similarity 63.5%; Pred. No. 1.4e-68; Mismatches 47; Indels 16; Gaps 4;
 Matches 148; Conservative 63.5%; Pred. No. 1.4e-68; Mismatches 47; Indels 16; Gaps 4;

Qy 7 SAPPSULLILQLVGRAAAASKAPVCQETVPMERGIGGNLTMPNQFNHDTOEAGLE 66
 11 SALALCVULLWSSVGR----EHVCOBISVPLCIGIGYNTYMPNQFNHDNEAGLE 64

Db 67 VHOFWPLVEIQCSPDLRFFLCTMYTPICLDPYHKPLPCCSVCEAKAGKAGSPLMRYQGRWPERM 126
 65 VHOFWPLVEIQCSPDLRFFLCSMYTPICLDPYKKPLPCCSVCEAKAGKAGSPLMRYQGRWPERM 124

Qy 127 WPERMSCDLPVLRDAEVLMYDYNRSEATTAPPRP---PAKTLPGPPGAPASGGEC 182
 11 SALALCVULLWSSVGR----EHVCOBISVPLCIGIGYNTYMPNQFNHDNEAGLE 64

Db 125 WPDNRWCDLIPVQDG-DPNTLCMDYNTDATSSPAKPTTSRPGKPKRNKNSSPGSSCE 183

Qy 183 PAGGPVFCVKCEREPVPIKESHLINKRTGQFNCAPCVCYQPSFSADERTFA 235
 184 PE----CYCRAFPVPHSDHPLYNRVKTGQFNCAMPCHNPYLQSERTFA 231

RESULT 7
 Q9PWN8 PRELIMINARY; PRT; 576 AA.
 ID Q9PWN8
 AC Q9PWN8; DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

Db 67 VHOFWPLVEIQCSPDLRFFLCTMYTPICLDPYHKPLPCCSVCEAKAGKAGSPLMRYQGRWPERM 126
 65 VHOFWPLVEIQCSPDLRFFLCSMYTPICLDPYKKPLPCCSVCEAKAGKAGSPLMRYQGRWPERM 124

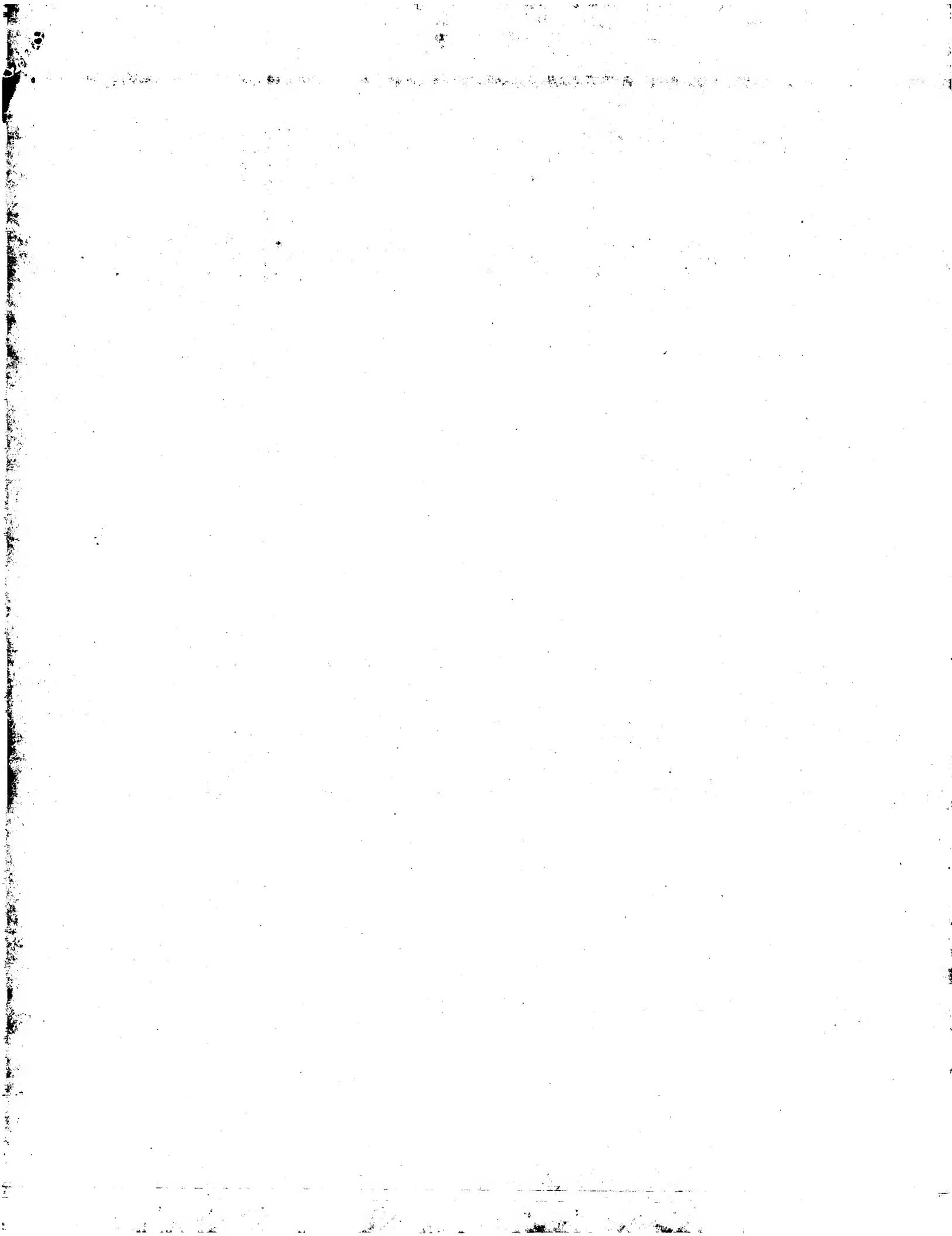
Qy 131 MSCDILUPVLRDAEVLCDMDNRSEATTAPRPFPRKPR-----TLPG 171
 ID :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db LSCEALPKMS-----DNSTGNICAAPPDTPKKKHKGHHQNQNQNHRHNSPDG 174
 Qy 172 PP-GPASGGCPCAG-GPPVCKCREPPVPIKESIPLYNKURTGQVNCAVPCQPSFS 228
 ID :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db PEVGISKIDNEVIAGPSECCTCNGQQPQFQVASE-----KSKVGVNTCAVSCHSPALA 227
 RESULT 10
 Q9YUJ7 PRELIMINARY; PRT; 550 AA.
 ID Q9YUJ7 PRELIMINARY; PRT; 550 AA.
 AC 09YUJ7
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
 DE Frizzled-2.
 DR ZF2Z.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC NCBI_TaxID=7955;
 RN [1]_SEQUENCE FROM N.A.
 RP RX MEDLINE=213369720; PubMed=11477685;
 RA Sunmara S., Kim H.J., Hermanson S., Ekker S.C.;
 RT "Zebrafish frizzled-2 morphant displays defects in body axis
 elongation,"
 RL Genesis 30:114-118(2001).
 EMBL: AY033592; AAC06401.1; -.
 DR IPR000539; Frizzled.
 DR InterPro; IPR00024; Fz domain.
 DR InterPro; IPR000832; GPCR secretin.
 PFam; PF01392; Fz; 1.
 DR PROSITE; PS5061; G PROBIN RECEP_P2.4; 1.
 DR PROSITE; PS5061; G PROBIN RECEP_P2.4; 1.
 SQ SEQUENCE; MW: 96568 MW; 980B08656B0D268C CRC64;

Query Match 32.8%; Score 429.5; DB 13; Length 550;
 Best Local Similarity .45.1%; Pred. No. 2.5e-33; Matches 87; Conservative 24; Mismatches 57; Indels 25; Gaps 8;

Matches 87; Conservative 24; Mismatches 57; Indels 25; Gaps 8;

Qy 33 CQEITVPMCRCIGNVLTHMPNQFNHDTOBAGLEHQFWPLVEIQCSPDILRFFLCTMYTP 92
 ID :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 39 CQPTRIPCLCDIAYVQTIMPLVGHYNQEQBAGLEHQFYPLVKVQCSPELKFFLSMYP 98
 Qy 93 ICLPPDHKPQPPCRVCYERAKAGCSPLMRQXGFAAHPERMCDRLVLTGRABEVICNDYR 152
 ID :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 99 VCTV-LEKAIPCRSICERAKQGCVELNKEFGQWPEALRCCEHFVWLGDHT-CVGQND 155
 Qy 153 SEATTAPPR-PFPAKT-IPGPPAPASGGCPCAGGPVCKCREPPVPIKESIPLYNK 209
 ID :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 156 SMATVSPVHMP1GPTPSVQLYSTPPDKPF--RCPS-----TLKV--PAYLS 196
 Qy 210 VRTGQVNPNCAVPC 222
 ID :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 197 YKFLGSPDCGAPC 209
 RESULT 11:
 Q9NL45 PRELIMINARY; PRT; 872 AA.
 ID Q9NL45
 AC Q9NL45;
 DT 01-OCT-2000 (T-EMBLrel. 15, Created)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Frizzled homolog.
 GN C1FRZ.
 OS Cliona intestinalis.
 OC Eukaryota; Metazoa; Chordata; Asciidae; Enterogona;
 OC Phleobranchia; Cionidae; Ciona.
 RN [1]_SEQUENCE FROM N.A.
 RP Emelyanov A., Sleptsova-Friedrich I., Fong I., Korzh V.;
 RT "Frizzled 7b interacts with Wnt5 in the enveloping layer of embryonic
 zebrafish,"
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF231123; AAC09481; -.
 DR InterPro; IPR00208; Aldehyde_dehydr.
 DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR00024; Fz domain.
 DR InterPro; IPR000832; GPCR secretin.
 DR PFam; PF01392; Fz; 1.
 DR PROSITE; PS0070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.

SQ	SEQUENCE	559 AA;	63695 MW;	85667E25AA50D82 CRC64;	Db	162 SDAGGPTSNPTPVWELITLQPNLVRPNQQFTCP-----LQLKVPTYL 205	
Query	Match	31.3%;	Score 410.5;	DB 13;	Length 559;	Qy	209 KVRTGQVNPNCAPC 222
Best Local Similarity	41.8%;	Pred. No. 1.	1.7e-31;			AC	08QFM3
Matches	81;	Conservative	25;	Mismatches	65;	DT	01-JUN-2002 (TREMBLrel. 21, Created)
AC	08QFM2;			Indels	23;	DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)
Db	45 QPISIPCLIDQIYNTIMPLNQLIGHTNQEDAGLEHQFPLVKVQCSMDLKFLCSMYAP 104			Gaps	4;	DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
Qy	33 COBITVPMRGIGYNYLTHMPQFNHDQTODAEGLEHQFPLVKVQCSMDLKFLCSMYAP 92					DE	Frizzled homolog 9 (Drosophila)
Db	93 ICLPDYHKPLPPCRSYCERAKGCSPLMROQGFAMPERMSCDRLPVGLGRDAEVLCMDYR 152					OS	Homo sapiens (Human).
Qy	105 VCTV-LEQAIIPCRSLCERAROGCEALMNKFQFWPLRCENFPVHG---AGEICVGONT 161					OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db	153 SEATTAPPRPFPAKTI---PGPGAPASGGCCPAGGPFWVKCRSPFPVILKEASHPLY 208					OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Qy	209 KVRTGQVNPNCAPC 222					OC	NCBI_TaxID=9605;
Db	206 KYHFMGEKDCGAPC 219					RN	SEQUENCE FROM N.A.
RESULT 13						RP	Sumaras S., Kim H.J., Hermanson S.B., Ekker S.C.,
09BSR2						RT	"Zebrafish frizzled-7A is expressed maternally and zygotically during
ID	Q9BSI2					RT	embryogenesis."
AC	Q9BSI2;					RL	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DT	01-JUN-2001 (TREMBLrel. 17, Created)					RN	[2]
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)					RP	SEQUENCE FROM N.A.
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)					RA	Emelyanov A., Sleptsova-Friedrich I., Fong I., Korzh V.,
DE	Frizzled 7 protein (Fragment);					RT	"Frizzled 7b interacts with Wnt5 in the enveloping layer of embryonic
GN	F27.					RT	zebrafish.";
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; OC					DR	Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; OC					DR	EMBL; AF437316; AAC07635_1; -
OC	Cyprinidae; Danio; NCBI_TaxID=7955;					SO	SEQUENCE FROM N.A.; 63475 MW; DEF32BF11159BC83 CRC64;
OX	NCBI_TaxID=7955;					RN	Sumaras S., Kim H.J., Hermanson S.B., Ekker S.C.,
RN	[1]					RT	"Zebrafish frizzled-7A is expressed maternally and zygotically during
RP	SEQUENCE FROM N.A.					RT	embryogenesis."
RX	MEDLINE=21184123; PubMed=11287199;					RL	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RA	El-Messaoudi S., Renucci A.,					RN	[2]
RT	"Expression pattern of the frizzled 7 gene during zebrafish embryonic development"; Mech. Dev. 102:231-234(2001).					RP	SEQUENCE FROM N.A.
RT	EMBL; AJ301617; CAC37335_1; -					RA	Emelyanov A., Sleptsova-Friedrich I., Fong I., Korzh V.,
RL	InterPro; IPR002086; Aldenzyde_dehydr.					RT	"Frizzled 7b interacts with Wnt5 in the enveloping layer of embryonic
DR	InterPro; IPR00539; Frizzled.					RT	zebrafish.";
DR	InterPro; IPR00024; Fz domain.					DR	Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR	InterPro; IPR00832; GPCR secretin.					DR	EMBL; AF336124; AAC0192_1; -
DR	InterPro; IPR01534; Frizzled; I.					SO	SEQUENCE FROM N.A.; 63475 MW; DEF32BF11159BC83 CRC64;
DR	PFam; PF01392; Fz; 1.					RN	Sumaras S., Kim H.J., Hermanson S.B., Ekker S.C.,
PRINTS	PRINTS; PR00489; FRIZZLED.					RT	"Zebrafish frizzled-7A is expressed maternally and zygotically during
SMART	SMART; SMM0063; FRI_1.					RT	embryogenesis."
PROSITE	PROSITE; PS00070; ALDHYDE_DEHYDR_CYS; UNKNOWN_1.					RL	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR	PROSITE; PS50038; FZ; 1.					RN	[2]
DR	PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.					RP	SEQUENCE FROM N.A.
FT	SEQUENCE 1					RC	SEQUENCE FROM N.A.
SQ	SEQUENCE 559 AA; 63719 MW; 25F243A465F04DAB CRC64;						
Query	Match	31.2%;	Score 408.5;	DB 13;	Length 559;	RESULT 15	
Best Local Similarity	41.8%;	Pred. No. 2.7e-31;				08TAN2	
Matches	81;	Conservative	25;	Mismatches	65;	ID	08TAN2
AC	08TAN2;			Indels	23;	PRELIMINARY;	PRT;
DT	01-JUN-2002 (TREMBLrel. 21, Created)			Gaps	4;	PRT;	591 AA.
Db	45 QPISIPCLIDQIYNTIMPLNQLIGHTNQEDAGLEHQFPLVKVQCSMDLKFLCSMYAP 104					DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)
Qy	33 COBITVPMRGIGYNYLTHMPQFNHDQTODAEGLEHQFPLVKVQCSMDLKFLCSMYAP 92					DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
Db	93 ICLPDYHKPLPPCRSYCERAKGCSPLMROQGFAMPERMSCDRLPVGLGRDAEVLCMDYR 152					DE	Frizzled homolog 9 (Drosophila)
Qy	105 VCTV-LEQAIIPCRSLCERAROGCEALMNKFQFWPLRCENFPVHG---AGEICVGONT 161					OS	Homo sapiens (Human).
Db	153 SEATTAPPRPFPAKTI---PGPGAPASGGCCPAGGPFWVKCRSPFPVILKEASHPLY 208					OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Qy	206 KYHFMGEKDCGAPC 219					OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Db	206 KYHFMGEKDCGAPC 219					OC	NCBI_TaxID=9605;
RC	SEQUENCE FROM N.A.					RN	SEQUENCE FROM N.A.
RC	TISSUE=BRAIN;					RP	SEQUENCE FROM N.A.



GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: May 22, 2003, 21:24:29 : Search time 2664 Second

256/.252 Million cell updates/sec

REFLECT SCORE: 1310
SEQUENCE: M A R P D P S A P P S I L I I I L A O I' P N C A V P C Y C O P S F A D E R T E A 23:0

Scoring table: BLOSUM62

Ygapop 10.0 **Ygapext** 0.5

DRAFT 6.0, Bantec / 1

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Minimum DB seg length: 0

Post-processing: Minimum Match

Listing first 45 81

Command line parameters:
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-Q=/cgn21/USPTO_spool/US09847102/runat190
-DB-CannE1_GMV-55555_GMIV-55555_VTWWV

-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -

-USER=US0984/102 @CGN 1 1_2496 @FHAT19052

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6

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6: gb_pat: *

46 88

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11:     gb_sts:*
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26: em_ko:
27: em_st8:
28: em_un:*

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29: em vi:*
30: em htg hum:*
31: em htg_inv:*
32: em htg_other:*
33: em htg_mus:*
34: em htg_pn:*
35: em htg_rod:*
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37: em htg_vrt:*
38: em sy:*
39: em htgo hum:*
40: em htgo mus:*
41: em_htgo_other:*

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SUMMARIES

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C	4	1250	95-4	179788	2	AC101915	AC101915 Mus muscu
C	5	1143	87-3	1734	10	AF272146	AF272146 Mus muscu
C	6	1131.5	86-4	746	9	HSA339758	AJ339758 Homo sapi
C	7	1017	77-6	821	9	HSA331422	AJ331422 Homo sapi
C	8	832.5	63-5	2380	5	AP300716	AF300716 Xenopus laevis
C	9	824	62-9	2085	6	AX367099	AX367099 Sequence
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C	11	824	62-9	166007	9	HSBA425A6	AJ121749 Human DNA
C	12	823.5	62-9	2421	10	MMU3321	U43321 Mus musculu
C	13	823.5	62-9	215585	2	AC103777	AC103777 Mus muscu
C	14	802	61-2	1851	5	AF017177	AF017177 Xenopus laevis
C	15	801	61-1	1740	5	AF117389	AF117389 Danio rerio
C	16	801	61-1	2249	5	AF060697	AF060697 Danio rerio
C	17	800	61-1	2554	5	AF039412	AF039412 Danio rerio
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C	19	796	60-8	3230	5	AF033110	AF033110 Xenopus laevis
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 Version U43318.1 GI:1151251
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 Organism Homo sapiens.
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 Title Wang, Y., Macke, J.P., Abella, B.S., Andreasson, K., Worley, P.,
 Gilbert, D.J., Copeland, N.G., Jenkins, N.A. and Nathans, J.
 Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and
 Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street,
 Baltimore, MD 21205
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 Authors Saitoh, T., Hirai, M. and Katoh, M.
 Title Molecular cloning and characterization of human Frizzled-5 gene on
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 Journal Int. J. Oncol. 19 (1), 105-110 (2001)
 Reference 2 (bases 1 to 3134)
 Authors Katoh, M.
 Title Direct Submission
 Submitted (24-MAY-2000) Masaru Katoh, National Cancer Center, Genetics Division, Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, Japan
 Fax: 81-3-3542-2511(ex.4402), (E-mail: mktoh@cc.go.jp), Tel. 81-3-3542-2511(ex.4402),
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AUTHORS			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE			Sulston, J.B. and Waterston, R.
PUBMED			Toward a complete human genome sequence
REFERENCE	2		Genome Res. 8 (11), 1097-1108 (1998)
AUTHORS			Belter, B., Cotton, M. and Spalding, M.
JOURNAL			The sequence of Homo sapiens BAC clone RP11-801F7
REFERENCE	3		Unpublished (2001)
AUTHORS			Waterson, R. H.
JOURNAL			Direct Submission
REFERENCE	4		Submitted (25-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
AUTHORS			(bases 1 to 177733)
JOURNAL			Waterson, R. H.
REFERENCE	5		Submitted (14-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
AUTHORS			Waterson, R. H.
JOURNAL			Direct Submission
REFERENCE	6		Submitted (15-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
AUTHORS			(bases 1 to 177733)
JOURNAL			Waterson, R. H.
COMMENT			Waterson, R. H.
			Direct Submission
			Submitted (23-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
			On Mar 14, 2002 this sequence version replaced gi:16604097.
			----- Genome Center
			Center: Washington University Genome Sequencing Center
			Center code: WUOSC
			Web site: http://genome.wustl.edu/gsc
			Contact: sapiens@watson.wustl.edu
			----- Summary Statistics
			Center project name: H_NH0801F07
			----- Drafting Center: WIBR

NOTICE:			This sequence was finished as follows unless otherwise noted:
			all regions were double stranded, sequenced with an alternate
			chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatsuno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR:

PBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-19cB10, 2000 bp overlap; the clone sequenced to the right is RP11-372C13, 2000 bp overlap. Actual end of this clone is at base position 22072 of RP11-372C13.

Polymorphisms have been identified between AC009409, AC079767, AC083900 and AC096772.

Data from AC009409 and AC022576 was used to finish this clone, AC096772.

The sequence of AC036191 has been incorporated into AC096772.

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Db	541 CACCGGCTCTACACACAGGTGGCAGGCCAGGGCGCTCGGGGGAGATGCC 480	QY 44 IleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAla 63
QY	224 GlnProSerProSerAlaAspGluArgThrPheAla 235.	Db 61 ATGGCTACACCTGACCCACATGCCAACAGTCACACAGACAGCAGGCG 120
Db	600 CAGCCGTA-CTTATTGGCGGAGGCCAGGTGCGA 634	QY 64 GlyLeuGluValHisGlnPheTrpProLeuValGluIleGlnCysSerProAspLeuArg 83
RESULT 7	HSA333422	Db 121 GCCTGGAGGGTCGACCACTCTGCCTGACATGCCAACAGTCACACAGACAGCAGGCG 120
LOCUS	HS333422	QY 84 PhePheLeuCysThrMetTyrThrProLeuValProAspTyrHisLysProLeuPro 103
DEFINITION	Homo sapiens genomic sequence surrounding NotI site, clone NL6-FM1R.	Db 181 TTCTTCCTATGCTCTAGTACACGCCATCTGCCCTACTACACAGCGCTGCG 240
ACCESSION	AJ333422	QY 104 ProCysArgSerValCysGluArgAlaLysAlaGlyCysSerProLeuMetArgInTyr 123
VERSION	AJ333422.1	Db 241 CCTGGCCCTCGGGAGTCGAGGCCACCCAGGCCCGCTGCTGGCGCTGATGCGCCAGTAC 300
KEYWORDS	GI:15877840	QY 124 GlyPheAlaIleTrpProGluArgMetSerCysAspArgLeuProValLeuGluIleArgPala 143
SOURCE	Homo sapiens.	Db 301 GACTTCCTCGGCCAGCCAGCCATGAGCTGGACCCCTCCCGGCTCTGGCCGCCAGGCC 360
ORGANISM	Homo sapiens	QY 144 GluValLeuCysMetAspTyrAsnArgSerGluAlaIleThrAlaProProArgPrope 163
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 821)	Db 361 GAGGTCCCTGCTGATGGATACACCGGAGGAGCCACAGGCCCTGGCGCTTC 420
AUTHORS	Kutsenko, A.S., Gitzullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M., Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V., Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I., Kiselev, L.L., Wasserman, W., Wahlestedt, C., and Zabavsky, E.R.	QY 164 ProAlaLysProThrLeuProGlyProProGlyAlaProAlaSerGlyGlyGlyCysPro 183
TITLE	NotI flanking sequences: a tool for gene discovery and verification of the human genome	Db 421 CCAGCCAGGCCACCCCTCCAGGCCGCCAGGGCGCTCGCGGAATGCTCC 480
RESULT 8	AP300716	QY 184 AlaGlyGlyProPheValCysLysCysArgGluProPheValProLeuLeuGluIleGlu 203
		Db 481 GTGGGGGCCCGTCGTCGTCGAGTGTGCGACGCCCTCTGGCCATTCTGAGGAGTC 540
		QY 204 HisProLeuTyrAsnIysValArgThrGlyGlnValProAsnCysAlaValProCysTyr 223
		Db 600 AGCTCGCT 608

LOCUS	AF00716	Xenopus laevis	2380 bp	mRNA	linear	WRT 09-MAY-2001	Qy	73	LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetTyrThrPro	92
DEFINITION		xenopus frizzled-5 mRNA, complete cds.					Db	394	TGGTGTGATCCAGTGTCACTGATTAAAGTTCTGTGAGCAGTACACT	453
ACCESION		AF00716					Qy	93	IleCysLeuProAspTYRHisLysProLeuProProCysArgSerValCysGluGala	112
VERSION		AF00716.1					Db	454	ATCGCTCTGCCGACTATAGGAAGCCTCTCCCTGGAGATGGCTGTGAGAAGAGCT	513
KEYWORDS		Xenopus laevis.					Qy	113	DYAlaGlyCysSerProLeuMetArgIntrgrgypheAlaTrpProGluArgMetSer	132
SOURCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xeropodinae; Xenopus.					Db	514	AAAGCGGATGTCCTCTCATGAGAAGATGGATTCTGGCCGGAGAGATGAC	573
REFERENCE		1 (bases 1 to 2380)					Qy	133	CyBapArgIleProValLeuIleArgAspAlaGluValLeuCysMetArgTyrArg	152
AUTHORS		Xenopus frizzled-5: a frizzled family member expressed exclusively in the neural retina of the developing eye.					Db	574	TGTGACCATGATGCCAGCATGGT---GACCGGATACTCTCATGATTAATTGG	630
JOURNAL		Mech. Dev. 103 (1-2), 133-136 (2001)					Qy	153	SergiuIalathThalaProProArgProHePheProlAlaProThrIleProGlyPro	172
MEDLINE		21233029					Db	631	ACTGAGAACCAACCCACTCGCCA-----CCCCACACCCCAA	672
PUBMED		1135120					Qy	173	ProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyGlyProHeValCys	192
2 (bases 1 to 2380)		Submitted (28-AUG-2000) Department of Genetics, Cell Biology and Development, University of Minnesota, 6-160 Jackson Hall, 321 Church St. SE, Minneapolis, MN 55455, USA					Db	673	GTAACACACCTACTAGT-----GACTGIGATGCC-----GTCTGCATATGC	714
FEATURES		source					Qy	193	ArgGluProHevalProIleLeuIleGluSerIleProLeuIleTyrAsnIleValArgThr	212
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CDS		178 . 1857					Qy	213	GlyGlnValProAsnCysAlaValProCysTyrginProSerPheSerAlaAspGlu	232
		/note="transmembrane receptor; xf25; putative Wnt receptor"					Db	775	GGCAGGCTAACCTACTGTGCTATGCCATGTTCCAGCCCCTACTTCACGAGGATGAA	834
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		TPHPKVKTPTPSDCGCKVCPFISIRESPLKPNLKGQVPCAMPQCPFTQDE								
		KMFTTFWGLWISICFISFTTIVAFILDMERPFYPERLTIFUSACYLFVLSIGVVR								
		IVGHEVNAVKNDHLYHETGPALITIVELLYPFGMASIIWVILWTFWLAGMKW								
		NEAATASYSOVFMHDYLWPSVLSKAVLAISVODPSVYDGYCYNQDNLDRFLVLP								
		LVVLFLPSGMWFLLQGFLVSFLRIRVKIQSGTKTKEKLMRIGLIFSVYTVRIVV								
		ACYVYEQHREHWSEITHNNSCPGKQKORYRDYAVFMLKTYLMCLVNGTISGWNTWSGK								
		LESWKRFTGRCCRPRINASAYEASRALTPTRGCLSNLTLPHQVPLSHV"								
BASE COUNT	637	a	522	c	530	g	691	t		
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Qy	33	CysGluGluIleThralProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro	52							
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ORIGIN										
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REFERENCE		/organism="Homo sapiens"								
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		Pred. No.:								
		1.91e-40	Length:	2085						
		Score:								
		824.00	Matches:	161						
		Percent Similarity:								
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		Query Match:								
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Db 505 ATTAATCGAACAAAAGAAAGGGGGGGGGGGCTGGACCCATAAGATAAGCCC 564
 Qy 182 CysProAlaGlyGlyProPheValCYSArgGluProPheValProIleLeuLys 201
 Db 565 TGGAGCCGGC-----TGCGAGTGTGCGGCCGATGGTGCCGTGAACAGC 612
 Qy 202 GluSerThrProLeuTyrAsnLysValArgTrpGlyGlnValProAsnCysAlaIlePro 221
 Db 613 GATCGACACCCTCTAACCCCGTTAGACCGGTCAATTCCAACTGCGCATGCCA 672
 Qy 222 CysTyrGlnProSerPheSerAlaAspGluArgThrPhe 234
 Db 673 TGTACACACCCATATTTCAGCAGGATGAGCGGACTTT 711

Search completed: May 23, 2003, 05:26:08
 Job time : 2758 secs

GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.

SUMMARIES

OM protein - nucleic search, using frame_plus_p2n model
Run on: May 22, 2003, 18:42:08 ; Search time 263 Seconds
(without alignments)
2012.242 Million cell updates/sec

Title: US-09-847-102a-68
Perfect score: 1310
Sequence: 1 MARPDPSAPPSSLLLQL..... PNCAVPQYQPSFSADERTPA 235

Scoring table:

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Ygapop 10.0 ; Ygapxt 0.5
Fgapop 6.0 ; Fgapxt 7.0
DelOp 6.0 , Delext 7.0

Searched:

2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=(cgn21/usPRO.spool)/US0947102/runat.19052003_160405_724/app.query.fasta_1.391
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
SUMMARIES					
1	1310	100.0	2334	18 AAT9889	Human frizzled gen
2	824	62.9	2085	24 ABK15174	Human RETTR 6 cDNA
3	823.5	62.9	2421	18 AAT9889	Mouse frizzled gen
4	754	57.6	424	24 ABL23141	Human ovarian canc
5	621	47.4	2085	23 ABL29961	Drosophila melanogaster frizzled
6	621	47.4	2344	18 AAT98885	Drosophila melanogaster frizzled
7	621	47.4	4085	23 ABL29960	Mouse frizzled gen
8	440.5	33.6	2259	18 AAT9889	Hydrophobic domain
9	415	31.7	1941	21 AAA60177	Human "frizzled" f
10	415	31.7	4485	21 AAA60189	Rat sequence diffe
11	398	30.4	4540	24 ABK6377	Human frizzled fam
12	397	29.5	2296	22 AAF15974	Human frizzled
13	380.5	29.0	1909	19 AAV13101	Human hoxD cDNA
14	380.5	29.0	1909	24 ABK64750	Human benign prost
15	380.5	29.0	2039	22 AAF80535	Colon adenocarcino
16	378	28.9	1893	19 AAV14017	Drosophila melanogaster
17	372.5	28.4	1484	19 AAV18254	Xenopus growth-ind
18	372.5	28.4	1920	21 AAA0573	Nucleotide sequenc
19	372.5	28.4	1920	21 AAA0573	Xenopus sp embryo
20	372.5	28.4	2039	22 AAF15973	Receptor #23 Parti
21	370.5	28.4	2621	22 AAF15973	Mouse frizzled fam
22	370	28.2	3847	23 ABL28857	Drosophila melanog
23	367.5	28.1	1291	19 AAV18255	Xenopus growth-ind
24	367.5	28.1	1786	19 AAV13102	Mouse hairz cDNA
25	367.5	28.1	2441	19 AAV13104	Mouse hoxZ cDNA (v
26	367	28.0	2176	24 AAV19691	Mouse "frizzled" f
27	367	28.0	2176	24 AAV18253	Mouse ischaemic co
28	366	27.9	2374	19 AAV14014	Bovine growth-indu
29	360	27.5	1975	16 AAV14014	Xenopus "frizzled"
30	349	26.6	1969	20 AAV80658	Partial human FRAZ
31	349	26.6	1969	22 AAC14496	Partial nucleotide
32	349	26.6	1969	24 ABQ8234	Human osteoblast d
33	349	26.6	5311	23 ABL28855	Drosophila melanog
34	342.5	26.1	1046	20 AAX86551	Nucleotide sequenc
35	342.5	26.1	1458	19 AAV08951	Human ARG-1639 pro
36	342.5	26.1	1581	20 AAX86556	Full length clone
37	342.5	26.1	1767	22 AAC94495	Human FRIZZLED pol
38	342.5	26.1	2009	22 AAF80598	Receptor #86 Parti
39	342	26.1	1041	21 AAA90464	Bos taurus Frizzle
40	339.5	25.9	1767	20 AAV0657	Human FRIZZLED pro
41	338.5	25.8	1041	21 AAA9128	Breast cancer prot
42	338.5	25.8	2820	24 ABL2118	Prostate cancer prot
43	338.5	25.8	2839	24 AAL11901	Human frizzled rel
44	338.5	25.8	2840	21 AAA5127	Breast cancer prot
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AC	AAT89889;				
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DT	27-APR-1998	(first entry)			
XX					
DE	Human frizzled gene 5 (Hfz5) encoding a Wnt receptor.				
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KW	Wnt receptor; human frizzled gene 5; Hfz5 gene; signal transduction; cancer; cell growth; cell proliferation; mammary tumour; oncogene; therapy; db.				
OS	Hom sapiens.				
XX					
PF	Location/Qualifiers				
CDS	321..2078				

PT FT
 XX WO9739357-A1.
 PN 23-OCT-1997.
 XX PR 11-APR-1997; 97WO-US06049.
 XX PR 12-APR-1997; 96US-0015307.
 XX PA (UWJO) UNIV JOHNS HOPKINS.
 PA (ISTRD) UNIV LEELAND STANFORD JUNIOR.
 XX PT Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J;
 PT Nusse R, Samos CH, Wangy;
 XX DR WPI; 1997-526631/48.
 XX PT-PADB; AAW31271.
 XX PT Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation related disorders
 XX PS Disclosure; Page 36-37; 61pp; English.
 CC This sequence comprises novel human frizzled gene 5 (Hfz5) that encodes a transmembrane receptor, frizzled-5 (see AAW31771), a Wnt receptor (WntR). Novel frizzled family members have been identified in Drosophila, mouse, human and Caenorhabditis (see AAT89885-92) and are considered to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.
 CC Sequence 2334 BP; 356 A; 803 C; 736 G; 439 T; 0 other;
 XX Pred. No.: 6.2e-84 Length: 2334
 Score: 1310.00 Matches: 235
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 18 Indels: 0
 DB: Gaps: 0
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 QY 21 ValIgYArgAlaAlaAlaAlaAlaLysAlaProValCysGlnGluIleThrAlaProMet 40
 DB 381 GtGGGCCGGGCCCCGGGCTCAAGGCCCGTGTGCCAGAAATCAGGTGCCATG 440
 QY 41 CysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
 DB 441 tGGCGCCGATCGCTACACAGCACGACGACATGCCAACACAGACACCGAG 500
 QY 61 AspGluIalaGlyLeuIuValIuHisGinPheTrProLeuValGluIleGlnCysSerPro 80
 DB 501 GAGGAGGGGCGCTGGAGGTGACCGAGTCAGCCGCGTGGAGATCCATGCTGGCG 560
 QY 81 AspLeuArgPheIleLeuCysThrMetYrrnProIleCysLeuProAspTyrIlys 100
 DB 561 GACCTGCCTCTTCCTGACTAGTACACCCATCTGTGCCGAGTACACAG 620
 QY 101 ProLeuProProAspSerValCysGluIgAlaLysAlaGlyCysSerProLeuMet 120
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QY 121 ArgGlnTyrglyPheAlaTrpProgluArgMetSerCysAspArgLeuProValLeuIgLy 140
 DB 681 CGCCAGTCAGCTGCTCCCTGCCCAGGGATGAGCTGCTCCGGTGCCTGGC 740
 QY 141 ArgAspAlaGluValLeuCysMetAspTyrasnArgSerGluAlaThrThrAlaProPro 160
 DB 741 CGCAGCCGGAGTCCTCTGCAAGGATACACCGAGCCAGGGCCACAGGGCC 800
 QY 161 ArgProProPheProAlaLysProThrIleProGlyProProGlyAlaProAlaSerGly 180
 DB 801 AGGCTTTCGGAGCCACCCCTCCAGGCCAGGCGCCAGGGCGCCACTGGCGGGC 860
 QY 181 GluCysProAlaGlyGlyProPheValCysLysCysArgGluProPheValProLeu 200
 DB 861 GAATGCCCGCTGGCGGCCGCTGCTGCTGAGTGTGCGAGCCCTTGRCGCCATTCCTG 920
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 QY 221 ProCysTyrGlnProSerProSerAlaAspGluArgThrPheAla 235
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 XX AC ABK15174;
 XX DT 23-APR-2002 (first entry)
 XX DE Human REPTR 6 cDNA sequence.
 XX KW REPTR; human; antiinflammatory; cytostatic; immunosuppressive; antiviral; anti-HIV; antiarthritic; anticonvulsant; nootropic; neuroprotective; anti-allergic; antibody; immunogen; endometriosis; KW gastrointestinal disorder; gastritis; oesophageal carcinoma; Crohn's disease; irritable bowel syndrome; ulcerative colitis; KW endocrine disorder; hypothalamus disorder; Kallman's disease; autoimmune disease; inflammatory disease; infertility; receptor; KW acquired immune deficiency syndrome; AIDS; rheumatoid arthritis; allergy; osteoarthritis; diabetes mellitus; multiple sclerosis; KW systemic lupus erythematosus; cell proliferative disorder; cancer; Becker muscular dystrophy; neurological disorder; epilepsy; gene; KW Alzheimer's disease; Huntington's disease; reproductive disorder; ss.
 XX OS Homo sapiens.
 XX FH Location/Qualifiers
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 FT CDS 1..2085
 FT /tag= a
 FT /product= "REPTR6 protein"
 XX PN WO200198354-A2.
 XX PD 27-DEC-2001.
 XX PF 21-JUN-2001; 2001WO-US19942.
 XX PR 21-JUN-2000; 2000US-214027P.
 XX PR 25-AUG-2000; 2000US-228045P.
 PR 12-DEC-2000; 2000US-255104P.
 XX PA (INCY-) INCYTE GENOMICS INC.
 XX PR Griffin JA, Kallick DA, Tribouley CM, Yue H, Nguyen DB, Tang YT;
 PR Lalai P, Policky JL, Azimzai Y, Lu DAM, Grauli R, Yao MG, Burford N;
 PR Hafaiia MA, Baugh MR, Bandman O, Patterson C, Yang J, Xu Y;
 PR Gandhi AR, Warren BA, Ding L, Sanjanwala MS, Duggan BM, Lu Y;
 PR

Page
4

CC identified in *Drosophila*, mouse, human and *Caenorhabditis* (see
 C C *ART9885-92*) and are considered to be Wnt receptors. Wnt receptors
 C C used in a novel, claimed method of screening for compounds
 which modulate the binding of a Wnt polypeptide (secreted proteins
 C C involved in cell-to-cell signalling) to a Wnt receptor. Wnt is
 involved in (mammalian) cancer and other processes involving growth,
 development and proliferation (both normal and abnormal).
 C C Modulators identified by the claimed method are useful for
 C C treatment of disease related to the conditions
 C C described above.

identified in *Drosophila*, mouse, human and *Caenorhabditis* (see AATR9895-92) and are considered to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.

```

Alignment Scores: 2.15e-49
      ref. NO.: 82350
      core: 69.06%
      percent Similarity: 60.00%
      best Local Similarity: 62.86%
      query Match: 18
      B: 8

Length: 2421
Matches: 159
Conservative: 24
Mismatches: 39
Indels: 43
Gaps: 8

```

S-09-847-102A-68 (1-235) x RAT89892 (1-2421)

Qy	230	AspGluIArgGlyThrPhe	234
Db			
	992	GATGAGCGCCCTTC	1006
RESULT 4			
ABL83141	ID	ABL83141 standard; cDNA; 424 BP.	
	ID	ABL83141	
	XX		
	AC		
	ABL83141;		
	XX		
DT	17-MAY-2002	(first entry)	
XX			
DE	Human ovarian cancer related cDNA clone SEQ ID NO:6119.		
XX			
KW	Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	W0200192581-A2.		
XX			
PD	06 - DSC-2001.		
XX			
PP	29-MAY-2001; 2001WO-US17756.		
XX			
PR	26-MAY-2000; 2000US-207484P.		
XX			
PA	(CORIXA) CORIXA CORP.		
XX			
PT	Algarte PA, Harlocker SL, Jones R;		
XX			
DR	WPI; 2002-122075/16.		
XX			
PT	Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide -		
XX			
PS	Claim 1; SEQ ID 6119; 489pp; English.		
XX			
CC	The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (III) of a ovarian tumour polypeptide encoded by a polynucleotide (III) having a cDNA sequence		
CC	polymerase encoded by a polynucleotide sequence as given in ABL77023 to		
CC	SL1) from the 1092 nucleotide sequences given in ABL77023 to		
CC	ABL87934, (III) encoding (II) having a sequence (S2), a T cell		
CC	population of (II), or antigen presenting cells that express (II).		
CC	(I) has cytostatic activity. An oligonucleotide (IV) that hybridises to		
CC	(S1) can be used for detecting ovarian cancer in a patient's biological		
CC	sample preferably serum or ovarian tissue. The method comprises		
CC	contracting a biological sample from a patient with (IV), detecting the		
CC	amount of polynucleotide hybridising to (IV) and comparing the amount to		
CC	a predetermined cutoff value and thereby detecting ovarian cancer in the		
CC	patient, where the amount of polynucleotide hybridising to (IV) is		
CC	detected preferably by polymerase chain reaction (PCR). (I) comprising		
CC	(III) and/or (II) is useful for stimulating and/or expanding T cells		
CC	specific for an ovarian tumour protein comprising contracting T cells		
CC	with (III) or (II). (III) is useful in design and preparation of		
CC	ribosome molecules for inhibiting expression of the tumour polypeptides		
CC	and proteins in tumour cells; and to isolate a full length gene from a		
CC	suitable library e.g., a tumour cDNA library using well known		
CC	techniques.		
XX			
SQ	Sequence 424 BP; 71 A; 163 C; 123 G; 67 T; 0 other;		
Alignment Scores:			
Pred. No.:	2.63e-45	Length:	424
Score:	754.00	Matches:	137
Percent Similarity:	97.8%	Conservative:	1
Best Local Similarity:	97.16%	Mismatches:	1
Query Match:	57.56%	Indels:	1
DB:	24	Gaps:	0

Qy 33 CysGlnGluLeuThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
 Db 2 TCCCAAGAAATCACGGGCCATGTGCCGCCATGGCTAACCTGACGCCAATGCC 61
 Qy 53 AsnGlnPheAsnHisAspThrGlnArgGluAlaGlyLeuGluValHisGlnPheThrPro 72
 Db 62 AACACGTCACACAGACACAGAGGAGGAGGGCTGGAGTGACCACTCGCCG 121
 Qy 73 LeuValGluIleGlyCysSerProAspLeuGlyPhePheLeuCysThrMetTyrThrPro 92
 Db 122 CTGGTGGAGATCAAATCTCGCGGACTGGCTTCATGCTATGCTACGCC 181

Qy 93 IleCysLeuProAspThrIleGlyProLeuProProCysArgSerValCysGluArgala 112
 Db 182 ATCTGTCGCGCGACTACACAGTCAGTCCTGCCGCCCTGCGTGAGGC-GCC 240
 Qy 113 LysAlaGlyCysSerProLeuMetArgGlnYrgIlePheAlaLrpProGluArgMetSer 132
 Db 241 AAGCCGCGTCTCGCGCTATGCCAGAACGCTGCGCCCTGCGTGAGGC-GCC 300
 Qy 133 CysAspArgLeuProValLeuGlyArgAspLauGluLeuCysMetAspTyrAsnArg 152
 Db 301 TCGACCGCTCCGGCTCTGGCCGGACCGAGCTCTCTGATGATTACACCG 360

Qy 153 SergiuAlathRthralaProProArgProLeuProLysProThrLeuProGlyPro 172
 Db 361 AGCGAGGCCAACACGGGCCCGCCAGCTTCCAGCCACCTTCCAGGCCG 420

Qy 173 Pro 173
 Db 421 CCA 423

RESULT 5
 ABL29961 ABL29961 standard; DNA; 2085 BP.

XX ABL29961;
 AC XX
 DT 26-MAR-2002 (First entry)

XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 41356.
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ds.
 OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 PR XX
 PD 27-SEP-2001.
 PR XX
 PR 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US1-19137P.
 PR 11-JUL-2000; 2000US-061450.
 PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR
 XX WPI; 2001-656860/75.

PS New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1676-ABL3051), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (AB05737-ABY2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fp.wipo.int/pub/published_pct_sequences.

XX Sequence 2085 BP; 405 A; 659 C; 614 G; 407 T; 0 other;

Alignment Scores:
 Pred. No.: 4.27e-35 Length: 2085
 Score: 621.00 Matches: 124
 Percent Similarity: 52.80% Conservative: 27
 Best Local Similarity: 43.36% Mismatches: 55
 Query Match: 47.40% Indels: 80
 DB: 23 Gaps: 7

US-09-847-102A-68 (1-235) x ABL29961 (1-2085)
 Qy 22 GlyArgAlaAlaAlaAlaAlaLysAlaPro-
 Db 118 GGTACGGCCCTGGACGCCGGAGTCCCACCCGGTTACGGAGTGCCAGTCATACCCAGGAT 177
 Qy 32 -----ValCysGlnGluLeuThrValProMetCysArgGlyIleGlyTyrAsnLeu 48
 Db 178 CCCAATTCGCGATGCGAGGAGATCACCATACCAATGTCGGGGCATTTGCTACTACAT 237
 Qy 49 ThrHisMetProAspGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHis 68
 Db 238 ACATCTTCCCCAAGAACATGACACCCAGGCAAGCGGCCCTGGAGSTGAC 297
 Qy 69 GluPhePheProLeuValGluIleGlyCysSerProAspLeuArgPhePheLeuCysThr 88
 Db 298 CGTTCTGGCCCTGGTGGAGATCAATACTGCGCGACCTCAAGTCTCTCTGCGAGC 357
 Qy 89 MetTyrThrProLeuProAspThrIleGlyProLeuProProCysArgSerVal 108
 Db 358 ATGTAACCGCCATCTGCTGGAGATTACCAACGCCGCGCCGTTGGCGAGTGT 417
 Qy 109 CysGluGuaGalaLysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaLrpPro 128
 Db 418 TCGCAGAGAGGCCGCTGGGATGCCAACCATCATGCCAGTACAGCTCGAATGGCCG 477
 Qy 129 GluAspMetSerCysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMet 148
 Db 478 GGAGAGATGGCTGGCGACGACTGCCCTCTCATGGT--GACCCGACAATCTGCGATG 534
 Qy 149 AspTyr----- 150
 Db 535 GRACACCCCTGTAACGGAGGCTGGCAAGCGCTGGCGGATCGGGTGCT 594
 Qy 150 ----- 150

Db 595 GGCAGCGGTCGGCTCAGGGCAAACGAAAGCAGGAGGAGGCACTGCGGGGGAGCT 654
 Qy 151 -----AspArgSerGluAlaThrThrAlaProProArgProProProLysLys 166
 Db 655 GGGGGGGCGCAGGGTTCCACCTCACGAAGCCTGGCGGGACCCAATCAA 714
 Qy 167 ProThrLeuProGlyProProGlyAlaProLysLeuGlyGlyGlyCysProAlaGlyGly 186
 Db 715 --AACTGCCAAATCCCCAGGAGAAAGCGCAAGCGAAAGACTGAGCTGAGC 762
 Qy 187 ProProValCysLysCysArgGluProProVal----- 197
 Db 763 -----TCTCTGGCCGCTCCCACTCATCTCTCTGGAGGAGGAGCTGAGCTGAGC 813
 Qy 198 -----ProLeuLeuLysGluUserHsBProLeuTyrAsnLysVal----- 210
 Db 814 CAGCAGTCGGAGATGCCCATGTCGACCATCCACCCAGCTGAGCTACTGTC 873
 Qy 211 --ArgThrGlyGlnValProAsnCysAlaValProCysTyrGlnProSerPheserAla 229

Db 1019 CAAAGCATCGCGGCTTCCAACTGGGCAATACCGTCAGGGCCCTCTTCAAGAAC 1078
 QY 230 AspGluArgThrPheAla 235
 Db 1079 GACGAAAGGATTGCC 1096

RESULT 7
 ABL2960
 ID ABL2960 standard; DNA; 4085 BP.

XX ABL2960;
 AC XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 41353.

XX KW pharmaceutical; gene; db.
 OS Drosophila melanogaster.
 PN WO20011042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PP 23-MAR-2001; 2001WO-US09231.
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.

XX PA (PEKE) PE CORP NY.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
 XX
 PS Claim 1; SEQ ID NO 41353; 2190 + Sequence Listing: English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1616-ABL3 051), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL5737-ABL2022).
 CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published.pct_sequences.
 CC
 SQ Sequence 4085 BP; 949 A; 1122 C; 1102 G; 912 T; 0 other;

Alignment Scores:
 Pred. No.: 9.05e-35 Length: 4085
 Score: 621.00 Matchers: 124
 Percent Similarity: 52.80% Conservative: 27
 Best Local Similarity: 47.36% Mismatches: 55
 Query Match: 47.40% Indels: 80
 DB: 23 Gaps: 7

US-09-847-102A-68 (1-235) x ABL29960 (1-4085)
 QY 22 GlyArgAlaAlaAlaLysAlaPro... 31
 DB 1118 GGTCAAGGCCTGGACCGGAGTCCGACCCGTTACGGAGTGCAGTCATACCCAGGAT 1177
 QY 32 - ValCysIleGluIleValPromtCysArgGlyIleGlyTyrAlanLeu 48

Db 1178 CCCAACTGGGATGGAGGATCACCAACATGGTGCGGGCATGGCTACAGATG 1237
 QY 49 ThrHisMetProAspGlnIpheAsnIleAspThrGlnIaspGluAlaGlyIleGluValHis 68
 Db 1238 ACATCCTCCCCAACGAATGACCATGAGACCCAGGACGAAGCGGGCTGGAGGTGCAC 1297

RESULT 7
 ABL2960
 ID ABL2960 standard; DNA; 4085 BP.

XX ABL2960;
 AC XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 41353.

XX KW pharmaceutical; gene; db.
 OS Drosophila melanogaster.
 PN WO20011042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PP 23-MAR-2001; 2001WO-US09231.
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.

XX PA (PEKE) PE CORP NY.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
 XX
 PS Claim 1; SEQ ID NO 41353; 2190 + Sequence Listing: English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1616-ABL3 051), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL5737-ABL2022).
 CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published.pct_sequences.
 CC
 SQ Sequence 4085 BP; 949 A; 1122 C; 1102 G; 912 T; 0 other;

Alignment Scores:
 Pred. No.: 9.05e-35 Length: 4085
 Score: 621.00 Matchers: 124
 Percent Similarity: 52.80% Conservative: 27
 Best Local Similarity: 47.36% Mismatches: 55
 Query Match: 47.40% Indels: 80
 DB: 23 Gaps: 7

US-09-847-102A-68 (1-235) x ABL29960 (1-4085)
 QY 22 GlyArgAlaAlaAlaLysAlaPro... 31
 DB 1118 GGTCAAGGCCTGGACCGGAGTCCGACCCGTTACGGAGTGCAGTCATACCCAGGAT 1177
 QY 32 - ValCysIleGluIleValPromtCysArgGlyIleGlyTyrAlanLeu 48

Db 1178 CCCAACTGGGATGGAGGATCACCAACATGGTGCGGGCATGGCTACAGATG 1237
 QY 49 ThrHisMetProAspGlnIpheAsnIleAspThrGlnIaspGluAlaGlyIleGluValHis 68
 Db 1238 ACATCCTCCCCAACGAATGACCATGAGACCCAGGACGAAGCGGGCTGGAGGTGCAC 1297

Db 69 GluPheTrpProLeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThr 88
 QY 1298 CAGTCTGGCCCTGGTGGAGATCAAATGCTCGCCGGACCTCAACTCTCTGTCAG 1357

Db 89 MetTrpThrProLeuProLeuProSpTHisLYSProlLeuProProCysBargServal 108
 QY 1358 ATGTACAGGCCATCTGCCCTGGAGATACACAGCCCTGCCGTTCCGSAGTGGTC 1417

Db 109 CybGlugArgAlaLysAlaGlyCysSerProLeuMetArgGlnTrpGlyPheAlaTrpPro 128
 Db 1418 TGGAGAGACCCGCTGGATGCCACCATCATGAGCAGTAGCTGAATGGCG 1477

QY 129 GluArgMetSerCysAspArgLeuProValLeuIleGlyArgAspAlaGluValLeucySMet 148
 Db 1478 GAGAGATAGGCGTGCAGCACTGCTCTCATGTT--GACCCGACAATCTGIGCAT 1534

QY 149 AspTrp...: 150

Db 1535 GAAACGCCCTGTAACCGAGGGCTGGCAGCGGGGGATGGGGGGCT 1594

QY 150 ----- 150

Db 1595 GGCACGGGTTCCGGCTCCGGGCAAACGGAAAGCAGGAGGCACTGGCTGGGGGGCACT 1654

QY 151 -----AspArgSerGluIalaThrAlaProProArgProPheProProAlaLys 166
 Db 1655 GGGCCGGCGCGCAGCAGGGTTCCACCTCAACGAGCAGCCTGCCGGACCAATCAAA 1714

QY 167 ProThrLeuProGlyProProGlyAlaProAlaSerGlyIleGlyCysProAlaGlyGly 186
 Db 1715 ---AACTGCCAAATCCCCAGAGAACAGGAAAGGCAAGGAAAGAGTGCGAC----- 1762

QY 187 ProPheValCysLysCysArgGluProPheVal----- 197
 Db 1763 -----TCCTCTGCCCTCCCACTCATCTCTGGGAAGGGAGCAGCTGTCAG 1813

QY 198 -----ProIleLeuIysGluSerHsProlLeuTyRAsnIysVal----- 210
 Db 1814 CAGCACTGCGAGATGCCCATGACCATCCACACCACTGGTACATGAACTACTGRC 1873

QY 211 --AspGlyIleGlyIleValProAspCysAlaValProCysTyrGlnProSerPheserAla 229
 Db 1874 CAAGAGATCGCCGCGTCCAACTGGGCATACCGTGCAAGGGCCCTTCTCAGAAC 1933

QY 230 AspGluArgThrPheAla 235
 Db 1934 GACGAAAGGATTGCC 1951

Db AAT8981 standard; DNA; 2259 BP.

XX AAT8981;
 AC AAT8981;
 DT 27-APR-1998 (first entry)

XX Mouse frizzled gene 7 (Mfz7) encoding a Wnt receptor.

XX
 KW Wnt receptor; mouse frizzled gene 7; Mfz7 gene; signal transduction; cancer; cell growth; cell proliferation; mammary tumour; oncogene; therapy; db.
 KW mus musculus.
 PH Key
 FT CDS
 PT Location/Qualifiers
 *tag= a

PN	WO9739357-A1.	Qy	
XX	23-OCT-1997.	Db	745 CAGGGCTGCGAGCCTCATGACAAGTGTGGCTTCAGTGCCAGGGTTGGCTGC 804
PD		Qy	
XX		Db	134 AspargleuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrasnArgSer 153
PF	11-APR-1997; 97WO-US06049.	Qy	
XX		Db	805 GAAACTTCCCAGTCAGGT-----GCCGCGAGATCTGCTGSGCAGAACGTC 858
PR	12-APR-1996; 96US-0015307.	Qy	
XX	(UWJO) UNIV JOHNS HOPKINS.	Db	154 GluAlaThr-----ThraAlaproProArgProBpheProAlaLysProTyrasnLeuPro 170
PA	(STRD) UNIV LELAND STANFORD JUNIOR.	Qy	
XX		Db	859 GACGCTCGGG3GGCGGGCGAGTCCCACGCCPACCTRACTGTCCCTACCTGCCA 918
PI	Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J;	Qy	
XX	Nusse R, Santos CR, Wangy;	Db	171 GlyProProGlyAlaProAlaArgLysGlyGluCySProAlaGlyGly----- 1861
DR	WPI; 1997-526631/48.	Qy	
XX	P-PSDB; AAW31273.	Db	919 GACCCACCCATTCACTGGATGTC-----CCCTGATGGCAGAGCCGCTG 966
PS		Qy	
PT	Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation related disorders	Db	187 -----ProPheValCysLysCysArgGluProPheValProleuLysGluSerHis 2041
XX		Db	967 TCTTCCCTTCCTCTGCTGCG-----CGCACGTCAAAGTGCCC----- 1000
CC	This sequence comprises novel mouse frizzled gene 7 (Mfz7) that encodes a transmembrane receptor, frizzled-7 (see AAW31273), a Wnt receptor (WntR). Novel frizzled family members have been identified in <i>Drosophila</i> , mouse, human and <i>Caenorhabditis</i> (see AAT89895-92) and are considered to be Wnt receptors. Wnt receptors can be used in a novel claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.	Db	1060 CCCTACCTGGCTACCGCTTCTCTAGGTGAG---CGTACTGIGGTGCCCGTGT--GAG 1054
CC		Qy	
CC	Sequence 2259 BP; 362 A; 739 C; 677 G; 481 T; 0 other;	Db	225 ProSer-----PheSerAlaaspGluArgTrpRheala 235
SO		Qy	
Alignment Scores:		Db	1060 CCGGCCGCTGCTAACGGCTCTAGTACTTTAAAGAAGGAGAGACCGCTTCCC 1113
Pred. No.:	3.01e-22	Length:	2259
Score:	440.50	Matches:	100
Percent Similarity:	52.71%	Conservative:	36
Best Local Similarity:	38.76%	Mismatches:	75
Query Match:	33.63%	Indels:	47
DB:	18	Gaps:	12
US-09-047-102A-6B (1-235) x AAT89891 (1-2259)			
Qy	8 AlpProProSerIeuLeuLeuLeuLeuLeuAlaGlnLeuValGlyArgAlaAlaAla 27	XX	Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport; biophylaxis; signal receptor; ion channel; transporter; immunostimulant; immunosuppressant; haemopoiesis regulator; chemokinetic; haemostatic; thromboytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer; gene therapy; SS.
Db	391 TCGCCCTCTGGGCCCTGCCCCCTGGCTGCTGCCACCGAC 447	XX	
Qy	28 SerLysAlaPro-----ValCys 33	XX	
Db	448 ACCGGGCTCAGCCATATCACGGCGAGGAAGGCATCTCGGTACGGGACGCCGCTTCGC 507	PR	17-NOV-1998; 98JP-0326255.
Qy	34 GluGluIleThrValProMetCysArgGlyIleGlyTyRAsnLeuThrHisMetProAsn 53	PR	22-DEC-1998; 98JP-0364315.
Db	508 CAGCCCATCCTCCATCCCGTGTGCAAGGATAATGCCCTAACACGACCATCCGCCAC 567	PR	16-MAR-1999; 99JP-0069811.
Qy	54 GluPheAsnHisAspThrLeuAspPheGluAlaLysGluValHisGlnPheTerPProLeu 73	PR	21-APR-1999; 99JP-0119299.
Db	568 CTGCTGGGCCACAGAACAGAGGACCGGGCTCGAGTCACAGTCTACCTCTG 627	PR	19-MAY-1999; 99JP-0138169.
Qy	74 ValGluIleGlnCysSerProAspLeuArgPheLeuCysThrMetTyrThrProLeu 93	XX	
Db	628 GTAAAGGTCAGCTCTCTGAGCTACCTCTCTCTGCTATGCTGACCCGT 687	PA	(SAGA) SAGAMI CHEM RES CENT.
Qy	94 CysLeuProAspTyrHisLysProLeuProProAspArgSerValCysGluArgAlaLys 113	PA	(PROT-) PROTEGENE INC.
Db	TGACGCTG---CTGACGACCAAGCCATTCCCGCCGCTCTGAGCTGAGCCGCCGA 744	XX	Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic, hemostatic, thrombolytic -

OY	180	GlycylcysProAlaGly	Gly	ProAlaCysBarg	193
Db	778	GGGGCTTCCCGGCGGCCGCGCTGGAGCGGCAAGTCCTCTGCCG--CGC			834
OY	194	GluProPheValProLeuLysGluSerHisProLeuTyrAsnIvaLArgTrgGly			213
Db	835	GCCCTTAAGGTGCCCTACTCACTACCTGAGGAGAG			882
OY	214	GlnValProAspCysAlaValProCysTyrGlnProSer-----			226
Db	883	-----GAGTGGCGGCCACCTTG---GAGCCGACCAGGTGATGGCTCATGTC			930
OY	227	PheSerAlaAspGluArgThr-PheAla 235			
Db	931	TTCGGGCCGAGGAGCTGCCTCTCG 957			
RESULT 10					
AAA60189					
ID	AAA60189	standard; DNA; 4485 BP.			
XX					
AC					
XX					
DT	02-FEB-2001	(first entry)			
XX					
DE	Hydrophobic domain protein cDNA HP02539 isolated from Saos-2 cells.				
XX					
KW	Human; secreted protein; membrane protein; hydrophobic domain;				
KW	proliferation control; differentiation induction; material transport;				
KW	biophylaxis; signal receptor; ion channel; transporter; immunosimulant;				
KW	immunosuppressant; haemopoiesis regulator; chemotactic; chemokinetic;				
KW	haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;				
KW	autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer;				
KW	gene therapy; SB.				
XX	Homo sapiens.				
OS					
PA					
XX					
PN	WO200029446-A2.				
XX					
PD	25-MAY-2000.				
XX					
PF	17-NOV-1999;	99WO-JP06412.			
XX					
PR	17-NOV-1998;	98JP-0326255.			
PR	22-DEC-1998;	98JP-0364315.			
PR	16-MAR-1999;	99JP-0069811.			
PR	17-APR-1999;	99JP-0119999.			
PR	19-MAY-1999;	99JP-0138169.			
XX					
PA	(SAGA) SAGAMI CHEM RES CENT.				
XX					
PT	(PROT-) PROTEGENE INC.				
PT					
KATO	S. Kimura T;				
XX					
DR	WPI; 2000-38773/33.				
DR	P-PSDB; AAB12117.				
XX					
PT	Proteins comprising hydrophobic regions, such as secretory and membrane				
PT	proteins, useful in research and diagnostics and having various				
PT	activities e.g. immunomodulatory, antiinflammatory, chemokinetic,				
PT	hemostatic, thrombolytic -				
XX					
PS	Claim 4; Page 199-204; 410pp; English.				
XX					
CC	Secretory proteins play important roles in the proliferation control, the				
CC	differentiation induction, the material transport and the biophylaxis of				
CC	cells. Membrane proteins have important roles as signal receptors, ion				
CC	channels and transporters. The present sequence is the coding sequence				
CC	for a human protein which has at least one hydrophobic domain. The				
CC	protein encoded by the present sequence may be a secretory or a membrane				
CC	protein. The encoded protein may have cytokine and cell				
CC	proliferation/differentiation activity, tissue growth activity, immune stimulating or suppressing				
CC	activity, haemopoiesis activity, chemotactic/chemokinetic activity, haemostatic				
CC	activitiv/inhibit activity.				

CC prediction or identification of the physiological state of tissue or cell
 CC sample that has been exposed to a compound or agent. Hepatotoxicity
 CC is characterised by centrilobular necrosis and steatosis. The present
 CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
 CC which is differentially expressed in response to a hepatotoxic agent.

SQ Sequence 4540 BP; 998 A; 1255 C; 1220 G; 1067 T; 0 other;

Alignment Scores:

Pred. No.: 6.8e-19 length: 4540

Score: 398.00 Matches: 88

Percent Similarity: 53.70% Conservative: 28

Best Local Similarity: 40.74% Mismatches: 74

Query Match: 39.38% Indels: 26

DB: 24 Gaps:

US-09-847-102A-68 (1-235) x ABK63777 (1-4540)

Qy 33 CysGlnIleThrValProMetCysArgGlyIleLeuTyrAsnLeuThrHisMetPro 52

Db 1096 TGTCAGCCATTCATCCATCGCTGTGACGACATCGCTACATCAGACCATCGCC 1155

Qy 53 ArgGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPhePro 72

Db 1156 AACCTGGTGGCCACAGAACAGGAGACCGGGCCGGGGTGACCAAGTCACCG 1215

Qy 73 LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCystThrMetTyrThrPro 92

Db 1216 TTAGTGAAGGTCAGTCAGCGAGCTCTCTCTGCTCATGAGCTGCCT 1275

Qy 93 IleCysLeuProAspTyrHisLysProLeuProProCysArgSerValCysGluArgAla 112

Db 1276 GIGTGACGGATA---CTGGAGCAGGCCTGCCCCCTCCCTGCTCTGCTCCATGAGCC 1332

Qy 113 LysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArgMetSer 132

Db 1333 CAG---GGCTGGAGGCACTCTGAACAAGTRGGCTTCCAGTGGCCAGAACGCTCAAG 1389

Qy 133 CysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAsnArg 152

Db 1390 TCGGAGAGTTCCTGTCACAGCC-----SCGGAGAGCTTGCGTGGCCAGAACT 1443

Qy 153 SerGlnIleThrAlaProProArgProPheProAlaLysProThrLeuProGlyPro 172

Db 1444 TCGGACAAGGACCCGACTCTCTCTGCTGCCGGAGTCTGGACCAGCAATCCGAG 1503

Qy 173 ProGlyAlaProAlaSerGlyGlyGluCysProAlaGly-----Gly 186

Db 1504 CACGGCCGCGGTTACCGCGCGGCTACCGGGGAGTGGGGCCCGTGAGCGGGAA 1563

Qy 187 ProPheValCysIlysCysBargGluProPheValProLeuLeuGluSerHisProLeu 206

Db 1564 ANGTCCTCTGCGG----CGCCCTCTAGGGGTTCTCTACTCAACTACTCTG 1620

Qy 207 TyrAsnIysValArgThrGlyGlnValProAsnCysAlaValProCysTyrGlnProLeu 226

Db 1621 GGGGAGAG-----GACTGCGCGGCCCTGC--GAACCCACT 1656

Qy 227 -----PhesSerAlaGlyPheGluArgThrPheAla 235

Db 1657 AAAGTATAGGGCTCATGTCAGTCAGGGCTGCGCTTTCTG 1704

RESULT 12

AAF75974 standard; cDNA; 3269 BP.

XX AAF75974;

DT 22-MAY-2001 (first entry)

XX Human frizzled family gene 584 cDNA.

XX Human; frizzled family gene 584; embryo; foetus; cancer;

FW drug discovery; cytostatic; ss.

XX Homo sapiens.

OS WO200112808-A1.

PN 22-FBB-2001.

XX PF 18-AUG-2000; 2000WO-JP05552.

XX PR 18-AUG-1999; 99JP-0232018.

PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX PI Senoo C, Numata M;

XX DR WPI; 2001-211220/21.

DR P-PSDB; AAB37708.

XX PT WPI; 2001-211220/21.

XX PT as well as in cancer cells, useful in drug development for diseases

XX with abnormal expression including tumor -

Claim 1; Fig 6-7; 39pp; Japanese.

The invention relates to a novel frizzled family genes, 584, from mouse and human (cDNAs given in AAF5973 and AAF75974), and to the mouse and human 584 proteins (AAF73307, AAF73308). Gene 584 is strongly expressed in the embryo and foetus, and is also strongly expressed in cancer cells. The invention also relates to recombinant vectors and host cells comprising gene 584 nucleic acids, the recombinant expression of the 584 protein, methods of screening for modulators of 584 activity or expression, and the compounds thus identified. The human and mouse 584 genes represent a novel gene target for the development of drugs useful in the treatment of diseases such as cancer. The present sequence represents human gene 584 cDNA.

XX CC

CC Novel frizzled family genes 584 strongly expressed in embryo and fetus

CC as well as in cancer cells, useful in drug development for diseases

CC with abnormal expression including tumor -

XX CC

CC The invention relates to a novel frizzled family gene, 584, from mouse

CC and human (cDNAs given in AAF5973 and AAF75974), and to the mouse and

CC human 584 proteins (AAF73307, AAF73308). Gene 584 is strongly expressed

CC in the embryo and foetus, and is also strongly expressed in cancer

CC cells. The invention also relates to recombinant vectors and host

CC cells comprising gene 584 nucleic acids, the recombinant expression of

CC the 584 protein, methods of screening for modulators of 584 activity or

CC expression, and the compounds thus identified. The human and mouse

CC genes represent a novel gene target for the development of drugs useful

CC in the treatment of diseases such as cancer. The present sequence

CC represents human gene 584 cDNA.

SQ Sequence 3269 BP; 688 A; 961 C; 941 G; 668 T; 11 other;

Alignment Scores:

Pred. No.: 2.84e-18 length: 3269

Score: 387.00 Matches: 88

Percent Similarity: 50.88% Conservative: 28

Best Local Similarity: 38.60% Mismatches: 71

Query Match: 29.54% Indels: 42

DB: 22 Gaps:

US-09-847-102A-68 (1-235) x AAF75974 (1-3269)

Qy 1 MetalAlaArgProAspProSerAlaProProSerLeuLeuLeuLeuLeuLeuAlaGlnLeu 20

Db 486 ATGCAAGCCGGGGCCCCCG-----CTGGAAGCTGCTGAGCTG 527

Qy 21 ValGlyArgAlaAlaAlaAlaSerLysAlaProAla-----CYS 33

Db 528 ATGGGCTGAGCCGCCCCATGAGCTCCATGGACATGGAGCCCCGGGACGGCAATGC 587

Qy 34 GlnGluIleThrValProMetCysArgGlyIleLeuTyrAsnLeuThrHisMetProLeu 53

Db 588 CAAGCCATGAGATCCGATGTCGAGCATGGCTACATGAGCTGATGGCTGATGCAC 647

Qy 54 GlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpProLeu 73

Db 648 CTGATGGCCACAGAACCCAGGACGACGCGACGACGACGACGACGCTG 707

Qy 74 ValGluIleThrValProMetCysArgGlyIleLeuTyrAsnLeuThrHisMetProLeu 93

Db 708 GTGGACTTACGACTGCCACGGGACTCCGCTCTCTGAGCTGAGCTGAGCTG 767

Qy 94 CysLeuProAspTyrHisLysProLeuProSerValCysGluArgAlaLys 113

Db 768 TGCACGGAGCAGGTCTTACCCCTACCCCTCTGAGGGTATGTCGAGGCCCG 827

QY	114 AlaGlyCysSerProLeuMetArgGlnTyrglyPheAlaTrpProGluArgMetCys 133	Alignment Scores:	4.51e-18	length:	1909
Db	828 CTCAGATGTTCCCATATTGGACAGTCACTCACTGCCCCACTCCCTGACGCC 887	Pred. No.:	380.50	Matches:	83
Db	134 AspArgLeuproValLeuIgLyArgAspAlaGluValLeuCysMetAsp 151	Score:	50.00%	Conservative:	35
QY	888 CGGAACTCCC--AACAGAACGCCAACTACTGCGATGGAGGCCAACAC 944	Percent Similarity:	35.17%	Mismatches:	83
Db	152 ArgSerGluAlaThrAlaProProArgProheProAlaLys--ProThrLeuPro 170	Best Local Similarity:	29.05%	Indels:	35
QY	945 GGCTCGGACGAGGCCACCGGGCTCGGG-CCTGTCCGGCCGCTGTCGGCCAGC 1003	Query Match:	19	Gaps:	8
Db	171 GlyPro-----ProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyGlyProHe 188	DB:			
QY	1004 GCCCCACAGGGGGAGGACACCCGCTGAGGA-----Cggggccccgg 1048	US-09-847-102A-68 (1-235) x AAV13101 (1-1909)			
Db	189 ValCysLysCysArgGluProheValProleLeuLysGluSerHisProLeuTyRasn 208	QY	4 ProAspProSer-----AlaProProSerLeuLeuLeuLeuAla 18		
QY	1049 GCGGGCGGGCTGCGCAACACC----- 1069	Db	52 CCCATCCTGCCGGATCATGGGCTGGGGCACCCGGAGGAATGCGCTGCTGCGGCC 111		
Db	209 LysValArgThrGlyIglnValPro 216	QY	19 GluLeuValGlyArgAlaAla-----AlaAlaSerLysAlaProVal 32		
Db	1070 -----GGCAAGTCCA 1081	Db	112 GGCCTGCTGCCCTGGCTGCTCTGCTGCTGCCCTGGGCTGCGGTGEGCC 171		
RESULT 13	AAV13101	QY	33 CysGlnGluIleThrValProMetCysArgGlyIleGlyTyRasnHisMetPro 52		
ID	AAV13101 standard; cDNA; 1909 BP.	Do	172 TGTGAGCCGTCGCACTCCCCCTGIGCAAGTCGTCCTGCGCTGCTGCGCC 231		
XX	AAV13101;	QY	53 AspGlnPheAsnHisAspThrPheGlnAspGluAlaGlyIglnValHisGlnRheTpPro 72		
AC	DT 28-SEP-1998 (first entry)	Db	232 AACCAACCTGCACACAGCACTAGGACAACGCCATCCTGGCCATCGAGCAGTTCGAGGT 291		
DT	DE Human hsfz cDNA.	QY	73 LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetTyRhrPro 92		
XX	KW Human; nerve cell growth factor; hsfz protein; neuronal cell; proliferation; differentiation factor; ss.	Db	292 CTCTGGCACCCACTCAGCAGCCGATCTGCTCTCTGCTGCTGCGCC 351		
OS	Homo sapiens.	QY	93 IleCysLeuProAspTyr--HisLysProleuProProCysSerAlaSerValCysGluArg 111		
XX	Key 70..104 ^b	Db	352 ATCTGCACCATGACTCAGGACGAGCCCCATCAAGGCCATGTAAGCTGTTAGCTGCGAGCG 411		
FH	CDS /tag= b	QY	112 AlanalysAlaGlyCysSerProLeuMetArgGluLeuIgLyArgIglnValHisGlnRheTpPro 92		
FT	/product= hsfz	Db	412 GCGGGCAGGGCTGAGCCCTACTCATCAGTACGCCACTCGGCCATGCGCCAGAGAACCTG 471		
FT	DE19702835-A1.	QY	132 SerCysAspArgLeuProValLeuIgLyArgAspAlaGluValLeuCysMetAspTyRasn 151		
XX	22-JAN-1998.	Db	472 GCCTGGGAGGACTGCCAGTGACGAGGGCC-----GTGPGCATC-----TCT 516		
XX	PR 27-JAN-1997; 97DE-1002835.	QY	152 ArgSerGluAlaThrAlaProProArgProheProAlaLysProThrLeuProGly 171		
XX	09-JUL-1996; 96DE-1027631.	Db	517 CCCGAGGCCATGTTACTGCGGACGGAGCTGTTCT----- 555		
PA	(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.	QY	172 ProProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyGlyProheValCysLys 191		
XX	Deutsch U, Drexler JCA, Lottspeich F, Mayr T, Risau W; Rohrer H; WPT; 1998-080906/09. DR P-PSDB; AAW41767.	Do	556 -----ATGATTCTAGTAGAACGAGCTAGGGCAAGCAGTGAAGCTGTAA 606		
XX	New nucleic acid encoding protein that increases neuronal cell proliferation - useful as nerve growth factor and for detection or inhibition of differentiation factors	QY	192 CysArgGluProheValProleLeuLysGluSerHisProLeu-----Tyr 207		
PS	Claim 1; Page 11; 27pp; German.	Db	607 TGTAG-----CCTTTAGAGCTACACAGAGACCTATTCCGGAACTATTAC 654		
XX	This sequence encodes the human hsfz protein. This protein is found to increase the proliferation of neuronal cells. Such proteins can be used as nerve growth factors and for the detection and/or inhibition of differentiation factors specifically those corresponding to the Drosophila melanogaster wingless or mouse int-1 type.	QY	208 AspIysValArgThrGlyIglnValProAsnCysAlaValProCysTyr 223		
PT	Sequence 1909 BP; 523 A; 441 C; 437 G; 507 T; 1 other;	Db	655 ACTATGICATCGGGCTAAAGTTAAAGAGATAAGACTAAGTGCCAT 702		
CC	CC	RESULT 14			
CC	CC	ARK64750			
CC	CC	ID ASK64750 standard; DNA; 1909 BP.			
CC	CC	XX ABK64750;			
CC	CC	XX DT 18-JUN-2002 (first entry)			
CC	CC	DE Human benign prostatic hyperplasia gene #645.			
CC	CC	XX Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.			
CC	CC	OS Homo sapiens.			
SQ	SQ	XX			

PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235809P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236142P.
 PR 29-SEP-2000; 2000US-236819P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237395P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237479P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244667P.
 PR 01-Nov-2000; 2000US-245084P.
 XX PA (AVAL-) AVALON PHARM.
 XX YOUNG PE, Augustus M., Cart:
 PI Soppet DR, Weaver Z;
 XX DR
 WPI: 2002-188164/24.
 XX
 PT Screening for anti-neoplastic
 PT chemical agent to be tested
 PT determining a change in expr
 XX
 PS Claim 1; SEQ ID 282; 44PP; E1
 The present invention describes
 anti-neoplastic agent. The m
 agent to be tested for anti-
 neoplastic activity and can be used in
 expression of at least one g
 comprises a sequence (S) sell
 to ABT70110), or is at least
 expression is indicative of
 anti-neoplastic agent, and
 an anti-neoplastic agent, and
 is the data collected with
 result of M1, and the data i
 structure and/or properties
 treatment of cancer such as
 oesophageal, ovarian, kidney
 adenocarcinoma, carcinoma, c
 infiltrating lobular cancer,
 carcinoma, papillary carcinoo
 XX SQ Sequence 1909 BP; 523 A; 441

Length: 1909
 Matches: 83
 Conservative: 35
 Mismatches: 83
 Indels: 35
 Gaps: 8

PT Young E B, Augustus M, Carter RC, Boner K, Endress G, Holligan S;
PI DR Soppet DR, Weaver Z;
XX DR
WPI: 2002-188264/24.

XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set
XX

PS Claim 1; SEQ ID 282; 44pp; English.

XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of signature gene set, where (I) is
CC comprised of a sequence (S1) selected from 8447 sequences (given in AB10110,
CC to AB10110), or is at least 95% identical to (S1), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer, infiltrating ductal carcinoma,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumour.

Sequence 1909 BP; 523 A; 441 C; 437 G; 507 T; 1 other:
SQ XX

PR 27-SEP-2000; 20000US-231711P.
PR 27-SEP-2000; 20000US-235720P.
PR 27-SEP-2000; 20000US-238840P.
PR 27-SEP-2000; 20000US-231863P.
PR 28-SEP-2000; 20000US-236028P.
PR 28-SEP-2000; 20000US-236332P.
PR 28-SEP-2000; 20000US-236033P.
PR 28-SEP-2000; 20000US-236340P.
PR 28-SEP-2000; 20000US-236309P.
PR 28-SEP-2000; 20000US-236111P.
PR 29-SEP-2000; 20000US-236442P.
PR 29-SEP-2000; 20000US-236911P.
PR 02-OCT-2000; 20000US-237172P.
PR 02-OCT-2000; 20000US-2317173P.
PR 02-OCT-2000; 20000US-231278P.
PR 02-OCT-2000; 20000US-231294P.
PR 02-OCT-2000; 20000US-237295P.
PR 02-OCT-2000; 20000US-237316P.
PR 03-OCT-2000; 20000US-237425P.
PR 03-OCT-2000; 20000US-237598P.
PR 03-OCT-2000; 20000US-231604P.
PR 03-OCT-2000; 20000US-231606P.
PR 03-OCT-2000; 20000US-237608P.
PR 01-NOV-2000; 20000US-248867P.
PR 01-NOV-2000; 20000US-245084P.
XX (AVAIL-) AVALON PHARM.

Qy	19	GlnLeuIvalAlgyArgAlaAla-----AlaIaserLvaIlaPraloy	32
Db	33	CysGlcGluIleThrValProMetCysArgAlgyIleGlyTyrAsnLeuThrHisMetPro	52
Db	112	GeGCTGCGCCGCTGCGCTGCTCTGCCTGGGTGCCGGGCTCCGGCTGAGCC	171
Db	172	TGTGAGGCCGCGTCGCAACCCCTGTGCAAGTCCTGCTGGACTAGTGAATGAGCCC	231
Qy	53	AspGlnPheAsnHisAspSerThrGlnAspGluIlaAlgyLeuGluValAlaHisGlnPheThrPro	72
Qy	232	ANCCATGCGACACGACACTGAGGCCGAGCTGCTCTTCCTGCTGCCATCTGCCATCGAGGT	291
Db	73	LeuValGluIleLegIncySerProAspLeuArgPheLeuAlaCysThrMetTyrIlePro	92
Db	292	CTGCAGGACCCACCTGAGGCCGAGCTGCTCTTCCTGCTGCCATCTGCCATCGAGGT	351
Qy	93	IleCysLeuProAspTyr--HisLysProLeuProProCysAspSerValCysGluArg	111
Db	352	ATCTGACCATGACTTCAGCACGAGCCCTAACCCCTGAAAGCTGCTGCGAGCGG	411
Qy	112	AlaValAlaGlyCysSerProLeuMetArgLnyTyrGlyPheAlaLeuTrpProGluArgMet	131
Db	412	GCGCAGGGCTGTAAGCTGAGCCATACTCTCATGAGCTACGCCCTGCGGCCGAGAAGCTG	471
Qy	132	SerCysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAsn	151
Db	472	GCTGCGAGGACTGCGCACTGAGCAGACGAGGGCC-----GTGCGCATC-----TCT	516
Qy	152	ArgSerGluAlaIleThrAlaProProArgProPheProAlaIalySroThrIleProGly	171
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Qy	172	ProProGlyAlaProAlaSerGlyIlyGluCysProAlaGlyGlyProPheAlaCysLys	191
Db	556	-----ATGGATTCCTGATGCTGAGGAACTGAGCTGAGGGCCAGCAGCTGAAACGCTTAA	606
Db	192	CysBargGluProPheValProLeuLeuGluSerHisProLeu-----Tyr	207
Db	607	TGTAAAG-----CCUATTAGCTACAGAGAACCTATTTCGGAAACAATTAC	654
Qy	208	AspLysValArgThrGlyGlnValProAsnCysAlaValProCysTyr	223
Db	655	AACATGTCATTGGGCTAAAGTAAAGAGATAAGACTAAGTGCCAT	702

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 22, 2003, 18:09:48 ; Search time 55 Seconds
(without alignment(s))
1286.947 Million cell updates/sec

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DelOp 6.0 ; Delext 7.0

Searched:

441362 seqs, 153338381 residues
Total number of hits satisfying chosen parameters: 882724
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	% Match	Length	DB ID	Description
1	378	28.9	3893	3	US-08-878-414-10	Sequence 10, Appl
2	372.5	28.4	2039	4	US-09-276-531-45	Sequence 45, Appl
3	367	28.0	2176	3	US-08-878-414-8	Sequence 8, Appl
4	360	27.5	1875	3	US-08-878-414-4	Sequence 4, Appl
5	342.5	26.1	2009	4	US-09-276-531-108	Sequence 108, Appl
6	297	22.7	1796	4	US-09-216-531-113	Sequence 113, Appl
7	284.5	21.7	2030	4	US-08-837-057-1	Sequence 1, Appl
8	282	21.5	2833	4	US-09-276-531-23	Sequence 23, Appl
9	282	21.5	2880	2	US-08-987-289-1	Sequence 1, Appl
10	274.5	21.0	1984	4	US-08-837-057-5	Sequence 5, Appl
11	271	20.7	870	4	US-08-837-057-3	Sequence 3, Appl
12	18.8	1146	4	US-08-893-654B-5	Sequence 5, Appl	

RESULT 1

US-08-878-414-10 ; Sequence 10, Application US/08878474

; Patent No. 613322

GENERAL INFORMATION:

; APPLICANT: De Robertis, Edward M.
; APPLICANT: Boumeester, Tewig
; TITLE OF INVENTION: Endoderin, Cardiac and Neural Inducing
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4106

ALIGNMENTS

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,474
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6/0/020,150
FILING DATE: 20-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 3100.002US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/248-5500
TELEFAX: 415/362-5418

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1893 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-847-102a-10

Alignment Scores:

pred. No.:	3.9e-23
Score:	3.78.00
Percent Similarity:	49.79%
Best Local Similarity:	35.44%
Query Match:	28.85%
DB:	3

Length: 1893

Matches: 84

Conservative: 34

Mismatches: 83

Indels: 36

Gaps: 8

US-09-847-102a-68 (1-235) x US-09-878-474-10 (1-1893)

QY 4 ProAspProSerAla-----ProProSerIleLeuLeuLeuLeuLeu 17

Db 40 CCTGCCCATCTGGGATCAGTCCTGGCGAGCCGGGGATCTGCGG 99

QY 18 AlaGlnIleValGlyArgAlaAla-----AlaAlaSerlysAlaPro 31

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32 ValCysGlnGluIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrAsnMet 51

Db 160 GCGTGTGAGCCCTCCGATCCCTGCTGCAACTCCCTGGCCATCGAA 219

52 ProAspGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrp 71

220 CCCAACACCTGTCACACAGACTGAGCCATCTGGCCATCGAGTCGAA 279

QY 72 ProLeuValGluIleGlnCysSerProLeuProSpLeuArgPhePheLeuCysThrMetTyrThr 91

280 GCGTGCCTGGCACCCACTGCAAGCCATCTCTCTCTGCGCAATGAGCG 339

QY 92 ProIleCysLeuProAspTyr--HisLysProLeuProProCysArgSerValCysGlu 110

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460 CTGGCCCTGGAGGAGCTCCAGTGACGACGGC-----GCTGCGTC----- 504

151 AsnArgSerGluIalThrThrAlaProProArgProHeProAlaLysProThrLeuPro 170

505 TCTCCCGGGCCATCGTTACTGGGACCGAGCTGATTCTCT----- 546

QY 171 GlyProProGlyAlaProAspIleGlyGlyCysProAlaGlyGlyProHeValCys 190

547 -----ATGGATCTAGTAACTGGAACCTGTAGAGCTGGCAAGCAGTCGCTGT 594

QY 595 AAATGTAAG-----CTATTTAGGGTACACAGAGACCTATTCCGGACAAT 642

191 IlysCysTargGluProHeValProLeuIleGluSerHrsProLeu----- 206

QY 207 TyrAspLysValArgThrGlyGinValProAspCysAlaValProCysTyr 223

Db 643 TCACTATGTCATTCGGCTTAAGTAAAGAGATAAGAGCTAAGTGGCAT 693

RESULT 2

US-09-276-531-45

Sequence 45, Application US/09276531

Patent No. 6,839,688

GENERAL INFORMATION:

APPLICANT: Lal, Preeti

APPLICANT: Hillman, Jennifer L.

APPLICANT: Yue, Henry

APPLICANT: Reddy, Roopa

APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION

NUMBER OF SEQUENCES: 134

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCITE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/276,531

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/079,677

FILING DATE: March 27, 1998

CLASSIFICATION:

CLASSIFICATION: ATTORNEY/AGENT INFORMATION:

NAME: Lynn E. Murtry, Ph.D.

REGISTRATION NUMBER: 42,918

REFERENCE/DOCKET NUMBER: PA-0008 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 2039 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: MENTITU03

CLONE: 1256053

US-09-276-531-45

Alignment Scores:

pred. No.:	1.25e-22
Score:	372.50
Percent Similarity:	49.58%
Best Local Similarity:	34.75%
Query Match:	28.44%
DB:	4

Length: 2039

Matches: 82

Conservative: 35

Mismatches: 84

Indels: 35

Gaps: 8

US-09-847-102a-68 (1-235) x US-09-276-531-45 (1-2039)

QY 4 ProAspProSer-----AlaProProSerIleLeuLeuLeuLeuAla 18

Db 190 CCCATCTCTGGGGATCATGGTCTGGGGAGCCGGGGAGGGATECTGCTGGGGCC 249

QY 19 GlnLeuValGlyArgAlaAla-----AlaAlaSerlysAlaProVal 32

Db 250 GGGCTCTCTGCGCTGGCTGCTGCTCTGGCTGGGGCTGGGCTCGACCC 309

QY 33 CysGlnGluIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro 52

Db 310 TGTGACCCCTGGCTGGCTCCCTGGCAAGTCCCTGGGACATGAGTAGTCGCC 369

QY 53 AsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpPro 72

Db 370 AACCACTGACCAACGACATCAGGCCAGGCCATCTGGCCATGAGGAGTTCGAAGGT 429

QY 73 LeuValGluIleSerCysSerProAspLeuArgPhePheLeuCysSerMetTyrThrPro 92
Db 430 CTCCTGGCACCACTGCKGCCGATCTGCTCTCTGCGCATGTGCGCC 489
QY 93 IleCysLeuProAspTyr--HisLysProLeuProProCysArgSerValCysGluArg 111
Db 490 ATCTGCACTGACTTCCAGCAGGCCATCAAGTACCGCCACTCTGGCCGAGGG 549
QY 112 AlalaSlaGlyCysSerProLeuMetArgLysProTyrGlyPheAlaTrpProGluArgMet 131
Db 550 GCGCGCAGGCTGAGGCCATACTCATCAAGTACCGCCACTCTGGCCGAGGG 609
QY 132 SerCysApaPargLeuProValLeuGlyIleGlyAspAlaGluValLeuCysSerMetAspTyrAsn 151
Db 610 GCCTGCGAGGASCTGCGAGCAGGSC-----GTGTCATC-----TCT 654
QY 152 ArgSerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuProGly 171
Db 655 CGCGAGGCATCCTTACTCGGAGCAGCTGTTCT----- 693
QY 172 ProProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyLysProPheValCysIys 191
Db 694 -----ATGGATTCTCTAGTAACGGAAGCTGAGGGCAAGCAGTGAAACGCTGTAA 744
QY 192 CysArgGluProPheValProLeuLeuLysGluSerHisProLeu-----Tyr 207
Db 745 TGTAA-----CCTATTAGCTACAGAACCTATTCCGGACAATPAC 792
QY 208 AspLysValArgThrGlyGlyGlnValProAsnCysAlaValProCysTyr 223
Db 793 AACATGTCATCGGCTTAAGGTTAAAGAGATAAGACTAAGTCCAT 840

RESULT 3
US-08-878-474-B
; Sequence 8, Application US/08878474
; Patent No. 6133232
; GENERAL INFORMATION:
APPLICANT: De Robertis, Edward M.
TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,474
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,150
FILING DATE: 20-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 2B-758
REFERENCE/DOCKET NUMBER: 3100.002US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/248-5500
TELEFAX: 415/362-4118
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2176 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

QY 14 LeuLeuLeuLeuLysLagInLeuValGlyArgAlaAlaAlaAlaLysSerLysAlaProCys 141
Db 58 TGTCTAGCTCTGCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCA 58
QY 34 GluGluLleThrValProMetCysArgCysLysLysGlyLysTyrAlaLeuThrHisMet 178
Db 118 GACCTCTGTCGCGATCCGCTGCAAGGCTCTCCCTGGCCGGAGCTCAGGCTCA 118
QY 54 GlnPheAlaHisAspThrGlnAspGluLysGluLysGluLysGlnPheTyr 238
Db 178 CACCTGCAACACGACCAGCTGCAACGCTAACCCATCTGGCCATGGAACACTTCCGAA 178
QY 74 ValGluIleGlyCysSerProAspLeuArgPhePheLeuCysThrMetTyrThr 238
Db 238 CTGGCACCCACTGCGACCCGATCTCTCTCTCTCTGTCGAATGTCGA 238
QY 94 CysLeuProAspTyr--HisLysProLeuProProCysArgSerValCysGlu 298
Db 298 TGGACCATGCACTCCAGCACGACGCCATCAGCCCTGCAAGPCTGCTGAGG 298
QY 113 LysAlaGlyCysSerProLeuMetArgLysProTyrGlyPheAlaTrpProGluArg 358
Db 358 CGACAGGGCTGCGCCATTTCATCAAGTACCGCCACTCTGGCCGAGGCC 358
QY 133 CysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysSerMetAspTyr 418
Db 418 TGGGACGAGCTGCCGCGTACACCGGGCG-----GTGPGCATC----- 418
QY 153 SerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuProCys 499
Db 499 -----ATGGATGTCAGAFACTGAGACTGAGCAGTGGCAAGGGCAAGGAGCGAACGTTCC 499
QY 193 ArgGluProPheValProLeuLysGluSerHisProLeu----- 553
Db 553 AGG-----CCGGTCAAGGCTACACGAGCAAGACCTATCTGGAAACAT 553
QY 173 ProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyLysProPheValCys 601
Db 601 TATGTCATCCGGCTTAAGTTAAAGGTTAAAGATGAAATGTCAT 645

RESULT 4
US-08-878-474-4
; Sequence 4, Application US/08878474
; Patent No. 6133232
; GENERAL INFORMATION:
APPLICANT: De Robertis, Edward M.
TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California

Query Match: 26.15% Indels: 25
 DB: 4 Gaps: 6

US-09-847-102A-68 (1-235) x US-09-276-531-108 (1-2009)

QY 13 LeuLeuLeuLeuLeuLeuAlaGlnLeuValGlyArgAlaAlaAlaAlaLeuSerLysAlaProVal 32
 ::|||::|||::|||::|||::|||:
 Db 284 ATCCTAGTGGCCTGCGCTGTGCTGCACCTGGCGTGCGCTGGCGTGCGGGCGGCC--- 340
 ::|||::|||::|||::|||:
 QY 33 CysGlnGluIleThrValProMetCysArgGlyIleGlyTrpAsnLeuThrHisMetPro 52
 ::|||::|||::|||::|||:
 Db 341 TCCGAGCGGGTGGCACCCCTATGTCGCGCACATGCCTGCAACATCACCGATGCC 400
 ::|||::|||::|||:
 QY 53 AsnGlnIleAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnIlePheTrpPro 72
 ::|||::|||::|||:
 Db 401 AACCACTGCAACACAGCAGGAGAACCCATCTGGCATCAGACTAGAGGAG 460
 ::|||::|||::|||:
 QY 73 LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetTyrThrPro 92
 ::|||::|||::|||:
 Db 461 CGGTGGACGTCGAACTCGAGCCGCTGCGCTCTCCCTGTGCCATAGCGGCC 520
 ::|||::|||::|||:
 QY 93 IleCysBleuProAspTyr---HisLysProLeuProProCysArgSerValCysGluArg 111
 ::|||::|||::|||:
 Db 521 ATTGGAACCTCTGGAGTCCTGACGACCTCAAGCGTGAAGTGGTGTGCCAACGC 580
 ::|||::|||::|||:
 QY 112 AlanylAlaGlyCysSerProLeuMetArgInTrpProGluArgMet 131
 ::|||::|||::|||:
 Db 581 GCGGGCCACGACTGCGAGCCCTCATGAAAGTAGTACACCACTCGCCGAAAGCTG 640
 ::|||::|||::|||:
 QY 132 SerCysBspArgLeuProValLeuGlyArg-----AspAlaGluVal 145
 ::|||::|||::|||:
 Db 641 GCTGCGACGAGCTGCGTGTATGACCGTGGCGTCACCTCGCCGTGGCGAACCTG 700
 ::|||::|||::|||:
 QY 146 LeuCysMetAlaPtyrAsnArgSerGluAlaThrThrAlaProProArgProPheProAla 165
 ::|||::|||::|||:
 Db 701 AGGGACCTCCCGAGGGATGTTAGTGGATAACATCACAGACATGATGATCAGGAA 760
 ::|||::|||::|||:
 QY 166 LysProThrLeuProGlyProProGlyAlaProAlaSerGlyGlyGluCysProAlaGly 185
 ::|||::|||::|||:
 Db 761 AGGCCTCTT-----GATGTTGACTGAAACCCCTA 790
 ::|||::|||::|||:
 QY 186 GlyProPheValCysIleGlyArgGluProPheValProLeu----- 200
 ::|||::|||::|||:
 Db 791 AGCCCGCATCGTCGCAAGTGTAAG---GTAAGCCAACCTATCTCAGC 847
 ::|||::|||::|||:
 QY 201 ---LysGluLeuHisProLeuValAsnGluArgThrGlyGlyValProAsnCys 218
 ::|||::|||::|||:
 Db 848 AAAACTACAGCTATGTTATGCAAAATAAACTGTCAGAGGAGEGCTGC 904
 ::|||::|||::|||:
 RESULT 6
 US-09-276-531-113
 Sequence 113, Application US/09276531
 ; Parent No. 6183968
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Reddy, Roopa
 ; APPLICANT: Guigler, Karl J.
 ; APPLICANT: Baughn, Mariah R.
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
 ; NUMBER OF SEQUENCES: 134
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 33174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/276,531
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/079,677
 FILING DATE: March 27, 1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Lynn E. Murry, Ph.D.
 REGISTRATION NUMBER: 42,918
 REFERENCE/DOCKET NUMBER: PA-0008 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEX/FAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 113:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1796 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: ISINNOT01
 CLONE: 2375244
 US-09-276-531-113

Alignment Scores:
 Pred. No.: 2.52e-16 Length: 1796
 Percent Similarity: 297.00 Matches: 75
 Best Local Similarity: 46.45% Conservative: 23
 Query Match: 22.67% Mismatches: 69
 DB: 4 Indels: 44
 Gaps: 9

US-09-847-102A-68 (1-235) x US-09-276-531-113 (1-1796)

QY 33 CysGlnGluIleThrValProMetCysArgGlyIleGlyTrpAsnLeuThrHisMetPro 52
 ::|||::|||::|||:
 Db 799 TGTGAACCTATTACCTTACCTGAGATGTCGCAAGATTCCTCATGCCT 858
 ::|||::|||::|||:
 QY 53 AsnGlnIleAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnIlePheTrpPro 72
 ::|||::|||::|||:
 Db 859 AATCTCTTGATCATTTAGCAACAGACGAGCAGCTTGGCAATGGCCATTCCACCT 918
 ::|||::|||::|||:
 QY 73 LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetTyrThrPro 92
 ::|||::|||::|||:
 Db 919 ATGGGAACTCTGGATGTTCTGGGATTCGGCTTTCCTGCACTCTACGCTCT 978
 ::|||::|||::|||:
 QY 93 IleCysBleuProAspPheHisLysProLeuProProCysSerValCysGluAla 112
 ::|||::|||::|||:
 Db 979 ATTGTGTTG---GAATACTGGACGTCACACTCTCTGTGTCAGCTGGGGCT 1035
 ::|||::|||::|||:
 QY 113 LysAlaGlyCysSerProLeuMetArgInTrpProGluArgMetSer 132
 ::|||::|||::|||:
 Db 1036 TACAGTGAGTGTCTGAGCTCATGAGACTTGGTCTTGGCTTGAGATATGAA 1095
 ::|||::|||::|||:
 QY 133 CysBspArgLeuProValLeuGlyArgAspAlaGluValLeuCysNetLeuAspTyrAsnArg 152
 ::|||::|||::|||:
 Db 1096 TCCAGTRGGTCCCA-----GATTTGTTGAT----- 1119
 ::|||::|||::|||:
 QY 153 SerGluAlaThrAlaProProArgProPheProAlaLysProThrLeuProCys 172
 ::|||::|||::|||:
 Db 1120 -----GAGCCATATCTCGACTGTGGATCTGAATTAGCTGGAGAA 1161
 ::|||::|||::|||:
 QY 173 Pro---GlyAlaProAlaSer-----GlyGlyGluCysProAlaGly 185
 ::|||::|||::|||:
 Db 1162 CCAAATGAAAGGCCCACTGGCAGTCAGAGAGACTATGCTTTGCTCC---- 1215
 ::|||::|||::|||:
 QY 186 GlyProPheValCysIleGlyArgGluProPheValProIleLeuYsGluSerHisPro 205

QY 206 Leu---Ty---Asn---Val---Arg---Thr---Gly---Gln---Val---Pro---Asn---Cys---Ala---Val---Pro---Cys---Sty---Gln 224

Db 1240 CTGGCTTATTCCTTGCTG-----CATGTGCCTGATGTTCACTCTGTCACATTGCT 1290

QY 225 ProSerPheSerAlaAspGluArgThrPheAla 235

Db 1291 ATGTACTTCAGAAGGAAGAACGACTGTCATTGCT 1323

RESULT 7

Sequence 1, Application US/08937067

Patent No. 6433155

GENERAL INFORMATION:

APPLICANT: Umansky, Samuil

APPLICANT: Melkonyan, Hovsep

TITLE OF INVENTION: A FAMILY OF GENES ENCODING TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 812-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2030 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 253..1137

US-08-937-067-1

RESULT 8

Sequence 23, Application US/09276331

Patent No. 6183968

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Lal, Preti

APPLICANT: Hillman, Jennifer L.

APPLICANT: Yue, Henry

APPLICANT: Reddy, Rupa

APPLICANT: Guegler, Karl J.

APPLICANT: Baugh, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION

NUMBER OF SEQUENCES: 134

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/276,531

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/079,677

FILING DATE: March 27, 1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Lynn E. Murry, Ph.D.

REGISTRATION NUMBER: 42,918

REFERENCE DOCKET NUMBER: PA-0008 US

TELECOMMUNICATION INFORMATION:

US-09-847-102A-68 (1-235) x US-08-937-067-1 (1-2030)

QY 6 ProSerAlaProSerLeuLeuLeuLeuLeuAlaGln----- 19

Db 256 CGCGGGGGCCCTGCCTCGCTGCTGCTGCTGCCCTGCCTGCGCTGCACTGCTGCCCTGGCTCG 315

QY 20 -----LeuValGlyArgAlaAlaAlaAlaSerIleValAlaProValCysGln 34

Db 316 GCGCGGGGGCTCTCTCTCTCTGGCGAGCCGACTCTCTACAGGCGCGAGCTGCA 375

QY 35 GluLe-----ThrValProMetCysArgGlyIleGlyTyAspLeuThrHisMetPro 52

Db 376 CCCATCCCCGCCAACCTGCGAGCTGCGCACGCCATCCAGTAGTACAGAACATGGGGCTGCC 435

Db 53 AsnGlnPheAsnHiSapThrGlnAspGluAlaGlyIleGluValHiSglnPheTp-- 71

Db 436 ACTCTGCCTGGCCACGAGCTGAGGAGGTT---CTGACAGGGGGCCCTGGATT 492

Db 553 CGCTGCTGCTGCTGACGACTAGATGAGACCACTCAGCGCTGCACTGCTGCGTG 612

QY 72 ProteoValGluLileGlnCysSerProAspIleArgPhePheLeuCysThrMetTy-Thr 91

Db 493 CGCTGGCTCATGAGCTGCAACCCGGACACAAGAGTCCTGCTGCTGCTGCTG 552

Db 92 ProIleCysIleProAspTyRhslyProIleProProProCysArgServeralCysGluArg 111

Db 613 GTCAGGACCGGCTGCGCCGCGTCATGCTCCGCTTCGCTCCCTGCGACATGCTG 672

QY 132 SerCysAspArgIleProValIleGlyArgAlaGluValIleCysMetAspTyAsn 151

Db 673 GAGTGGCAGCCGTTCCCG-----CAGGAAACGAC-----CTCTCATCCCCCTGCT 720

QY 152 ArgSerGlu-AlaThrThrAlaProProArgProPhePro----AlaLysProThrLeu 169

Db 721 AGTAGCGACCACCTCTCCGGCACAGAGGAGCTCCAAAGGTGIGTGAAAGCCTGCAA 780

QY 169 uPro 170

Db 781 ACCA 784

TELEPHONE: (650) 945-4166
 FAX: (650) 945-4166
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2833 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: FBRRANT01
 CLONE: 150629
 US-09-276-531-23

Alignment Scores:
 Pred. No.: 8.33e-15 Length: 2833
 Score: 282.00 Matches: 65
 Percent Similarity: 41.23% Conservative: 22
 Best Local Similarity: 30.81% Mismatches: 80
 Query Match: 21.53% Indels: 44
 DB: 4 Gaps: 6

US-09-847-102A-68 (1-235) x US-09-276-531-23 (1-2833)

Qy 33 CysGlnGluLeuThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
 Db 241 TGTGAACTAACATTACTGTGCCAGATGATGAAATGGCTTACACAGTGAAGTTTCCT 300
 Qy 53 AsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpPro 72
 Db 301 AACATCTATGGCTCATATGACCAGAGTATGCCGCGTGGAAATGGAGCATTCCT 360
 Qy 73 LeuValGluIleGlyGlySerProLeuProGlyPhePheLeuCysGluValHisGlnPheMetTyrThrPro 92
 Db 361 CTGGCAAATCTGGATGTCACCAACATGGAACTTCCTCTGCAAGATTGTA 420
 Qy 93 IleCysLeuProAspTyrHisLysProLeuProProCysArgSerValCysGluGargAla 112
 Db 421 ACCTGCAATGACAACATCAT--GTTGGTTCACCTTGTCATAAACCTTGAGAGATA 477
 Qy 113 LysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheLeuLeuTyrProGluArgMetSer 132
 Db 478 TATTCGATGTCACAAATTATGGCACTTTGGGATCCGATGGAGCTTGAA 537
 Qy 133 CYSASPARGLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAsnArg 152
 Db 538 TGTGAACTAACATTACTGTGATGACTGTCTGTGA----- 576
 Qy 153 SerGluAlaThrThrAlaProProArgProPro-----ProAlaLysProThrLeuPro 170
 Db 577 -----ACTTTTGTATCCACACACAGAAATTCTGGTCCTCGGAAAGAAAACA----- 621
 Qy 171 GlyProProGlyAlaProAlaSerGlyGlyGlyCysProAlaGlyGlyProProValCys 190
 Db 622 -----GAACTGAACTGAAAGAGAGCTGGATTGGATTGGTGT 654
 Qy 191 LysCysArgGluProProValProIleLeuLysGluSerHisProLeuTyrAsnLysVal 210
 Db 655 -----CCAGGCACCTTAGACT 672
 Qy 211 ArgThrGlyGin-----ValProAsnCysAlaValProCysThrGlyGin 224
 Db 673 TCTGGGGGACAGGATAAGTTCTGGGAATGGCAAGCTGCGCCTCCATGCCAAC 732
 Qy 225 ProSerPheSerAlaLysPheGluArgThrPheAla 235
 Db 733 ATGTTTTAAAGGCTGAGCTAGGTTGCA 765

RESULT 9
 US-09-987-289-1
 ; Sequence 1, Application US/08987289
 ; Patent No. 5994098
 ; GENERAL INFORMATION:
 ; APPLICANT: HU, ERDING

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/987,289
 FILING DATE: 09-DEC-1997
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/048,725
 FILING DATE: 02-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: PRESTIA, PAUL F
 REFERENCE/DOCKET NUMBER: 23.031
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELEX: 846169

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2880 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-987-289-1

Alignment Scores:
 Pred. No.: 8.51e-15 Length: 2880
 Score: 282.00 Matches: 65
 Percent Similarity: 41.23% Conservative: 22
 Best Local Similarity: 30.81% Mismatches: 80
 Query Match: 21.53% Indels: 44
 DB: 2 Gaps: 6

US-09-847-102A-68 (1-235) x US-08-987-289-1 (1-2880)

Qy 33 CysGlnGluLeuThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
 Db 303 TGTGAACTAACATTACTGTGCCAGATGATGAAATGGCTTACACAGTGAAGTTTCCT 352
 Qy 53 AsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpPro 72
 Db 363 AACATCTATGGCTCATATGACCAGAGTATGCCGCGTGGAAATGGAGCATTCCT 422
 Qy 73 LeuValGluIleGlyGlySerProAspLeuArgPhePheLeuLysThrMetTyrThrPro 92
 Db 423 CTGGCAAATCTGGATGTCACCAACATGAACTTCCTCTGCAAGACATTGTA 482
 Qy 93 IleCysLeuProAspTyrHisLysProLeuProProCysArgSerValCysGluGargAla 112
 Db 483 ACTTCGATGAGAACATTATCAT--GTTGGTTCACCTTGCGTAACTTGTGAAAGATA 519
 Qy 113 LysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheLeuLeuTyrProGluArgMetSer 132
 Db 540 TATTCGATGTCACAAATTATGACACTTGGATGCCGATGGGCTGAGGGCTGAA 599
 Qy 133 CYSASPARGLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAsnArg 152
 Db 600 TGTGACAGATTACATACTGTGAGTAGCTGAGTTGCA----- 638

DB: 4 Gaps: 6

US-09-847-102A-68 (1-235) x US-08-937-067-5 (1-1984)

QY 153 SerGluAlaThrThrAlaProProArgProPhe----ProLalaLysProThrLeuPro 170

Db 639 -----AcTTTGATGCCACACAGAAATTCTTGGTCAGANGGAACA----- 683

QY 171 GlyProProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyGlyProProValCys 190

Db 684 -----GAACAGTCCAAAAGAGACATGGATTGGT 716

QY 191 LysCysArgGluProPheValProIleLeuLysGluSerHisProLeuTyRasnlysVal 210

Db 717 -----CCAGGCATCTTAAGCT 734

QY 211 ArgThrGlyGln-----ValProAsnCysAlaValProCysTyrGln 224

Db 735 TCGGGGGACAGGATAAGTTCTGGATGACCAGTGGCGCTCCATGCCAAC 794

QY 225 ProSerPheSerAlaAspGluArgThrPheAla 235

Db 795 ATGATTTAAAGTGTGAGCTAGAGTTGCA 827

RESULT 10

; Sequence 5, Application US/08937067

; Patent No. 643155

; GENERAL INFORMATION:

; APPLICANT: Umansky, Samuel

; TITLE OF INVENTION: A FAMILY OF GENES ENCODING METHODS OF USE THEREOF

; NUMBER OF SEQUENCES: 19

; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067

FILING DATE: 9-10-2000

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1984 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 216..1166

US-08-937-067-5

Alignment Scores:

pred. No.: 2.27e-14 Length: 1984

Score: 214.50 Matches: 69

Percent Similarity: 50.00% Conservative: 25

Best Local Similarity: 36.70% Mismatches: 71

Query Match: 20.95% Indels: 24

DB: 4 Gaps: 6

US-09-847-102A-68 (1-235) x US-08-937-067-5 (1-1984)

QY 17 LeuAlaGlnLeuValGlyArgAlaAla-Ala-----SerIysAlaProValCys 33

Db 314 CTACTATGGCTGGCAGGCCAGCCGCTCTACTCCAGCGCCAGTCAGTGGCTG 373

QY 33 sGlnGluLe-----ThrValProMetCysArgGlyIleGlyTyramineLeuThrHisMe 51

Db 374 CCTGACATCCGCGACCTGCCCTGCGCACAGGGCTCACAGGCATGGCT 433

QY 51 tProAsnGlnInpheAsnHisAspThrGlnAspGluLalaGlyLeuGluValHisGlnPhetr 71

Db 434 GCCAACACTGTGGAGGCCAGGAGCTGGCGAGGTGGAGCAGGGAGCAGTGCT 493

QY 71 pProLeuValGluLalaGlnCysSerProAspLeuProPhePheLeuCysthrMetTyrTh 91

Db 494 GCGCCTGCTGCCAAAGGCTGGTCACTGGTAGCAGCAGGCTTCGCGCTGCTGCTGCT 553

QY 91 tProLeuValGluLalaGlnCysSerProAspLeuProPhePheLeuCysthrMetTyrTh 111

Db 554 GCCCGCTGTC-----GACGGCCCATCTAACCGCCGCTCGTGGAGG 604

QY 111 GalAlaValGlyCysSerProLeuMetArgLntTyrGlyPheAlaLntProGluArgMe 131

Db 605 CGTGGGCCGCGCTGCGCGCTATGGAGGCCATGGCT 664

QY 131 tSerCysAspArgLeuProValLeuLysGluValLeu-CysMetAspTyrA 151

Db 665 GCACTGCCACAGTCCC--CTGACAAAGACCTCTGCTATGGCTGCT 711

QY 151 snArgSerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuPro 171

Db 712 -----AGTCGGCACCTGGCCGCCGCGC-----CTCCAGT 745

QY 171 LyProProGlyAlaProAlaSerGlyGlyCysProAlaGlyGlyProProValCys 191

Db 746 GACCAAGATCTCGGCCAGTGTGAGATG-GAGCACAGGTGACGCCCTATGGAGGAGA 804

QY 191 ysCysArgGluProPheVal 197

Db 805 TGTGCTCAGTGACTTGTG 824

RESULT 11

US-08-937-067-3

; Sequence 3, Application US/08937067

; Patent No. 6433155

; GENERAL INFORMATION:

; APPLICANT: Umansky, Samuel

; APPLICANT: Melkonyan, Hovsep

; TITLE OF INVENTION: A FAMILY OF GENES ENCODING METHODS OF USE THEREOF

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067

FILING DATE: 9-10-2000

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

Query Match: 18.36% Indels: 24
DB: 4 Gaps: 4

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 44..889
US-09-893-654B-1

Alignment Scores: 1.1e-10
Pred. No.: 231.50
Score: 50.60%
Percent Similarity: 30.95%
Best local Similarity: 17.67%
Query Match: 4

Length: 2190
Matches: 52
Conservative: 33
Mismatches: 66
Indels: 18
Gaps: 5

US-09-847-102A-68 (1-235) x US-09-893-654B-1 (1-2190)

Query 12 LeuLeuLeuLeuLeuAlaAglLeuValGlyArgAlaAla----- 26
Db 53 GTCCTCTGCCTCTCGCCATGCGCCGCCCTTGACATGGATA 112

Query 27 --AlaSerLysAlaProValCysGlnGluLeuThrValProMetCysArgGlyLeu 45
Db 113 TCCACCAAGTCGTTCCATGCCAAAGAGATGGC----ACTGCACTGCG 166

Query 46 TyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAla 65
Db 167 TACTGGAGATGGGTGCCCCATGACCCGCCAAT 537

Query 86 GluValHisGlnPheTrpProLeuValGlyArgAlaAla----- 26
Db 227 AAGTCAGCAGAGTGGCAGAACCTCTAACGACCGCTGCCCAGACCT 286

Query 86 GluValHisGlnPheTrpProLeuValGlyArgAlaAla----- 26
Db 287 CTATGTCCTCCATTGGCCCTAGTCCTGCTGACAGTC-----ACTCAGGCCCTGC 337

Query 106 ArgSerValCysGluArgAlaLysAlaGlyCysSerProLeuMetArgGlnArgGly 125
Db 338 CGCAGCATGCTGCTGCTGAAACAGITGTGCTCACITCTGCATCTGGCAC 397

Query 126 AlaTrpProGluArgMetSerCysAspArgLeuProValLeuAla----- 26
Db 398 TCCTGGCTGAGAGCTGAGCTGACGCTCCAGCT-----GGGGAGAC 445

Query 146 LeuCysMetAlaProValCysGlnGluLeuThrValProMetCysArgGlyLeu 45
Db 446 ATGTPGTCGACAC-TCTCGAAAGAGATATCGATGCTATAAAGA-----ACTGCC 498

Query 166 LysProThrLeuProGlyProPro 173
Db 499 AAAGCCAAGCTGCCAGGGCTGCC 522

RESULT 15

US-09-893-654B-1

; Sequence 1, Application US/08893654B

; Patent No. 616574B

; GENERAL INFORMATION:

; APPLICANT: RACIE, USA, ET ALIA

; TITLE OF INVENTION: Frazzled NUCLEOTIDE SEQUENCES, COMPOSITIONS AND USES

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESS: GENETICS INSTITUTE, INC.

; STREET: 87 CAMBRIDGE PARK DRIVE

; CITY: CAMBRIDGE

; STATE: MA

; COUNTRY: USA

; ZIP: 02140-2387

; COMPUTER READABLE FORM:

; COMPUTER TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/893,654B

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MEINERT, M.C.

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-498-8574

; TELEFAX: 617-876-5851

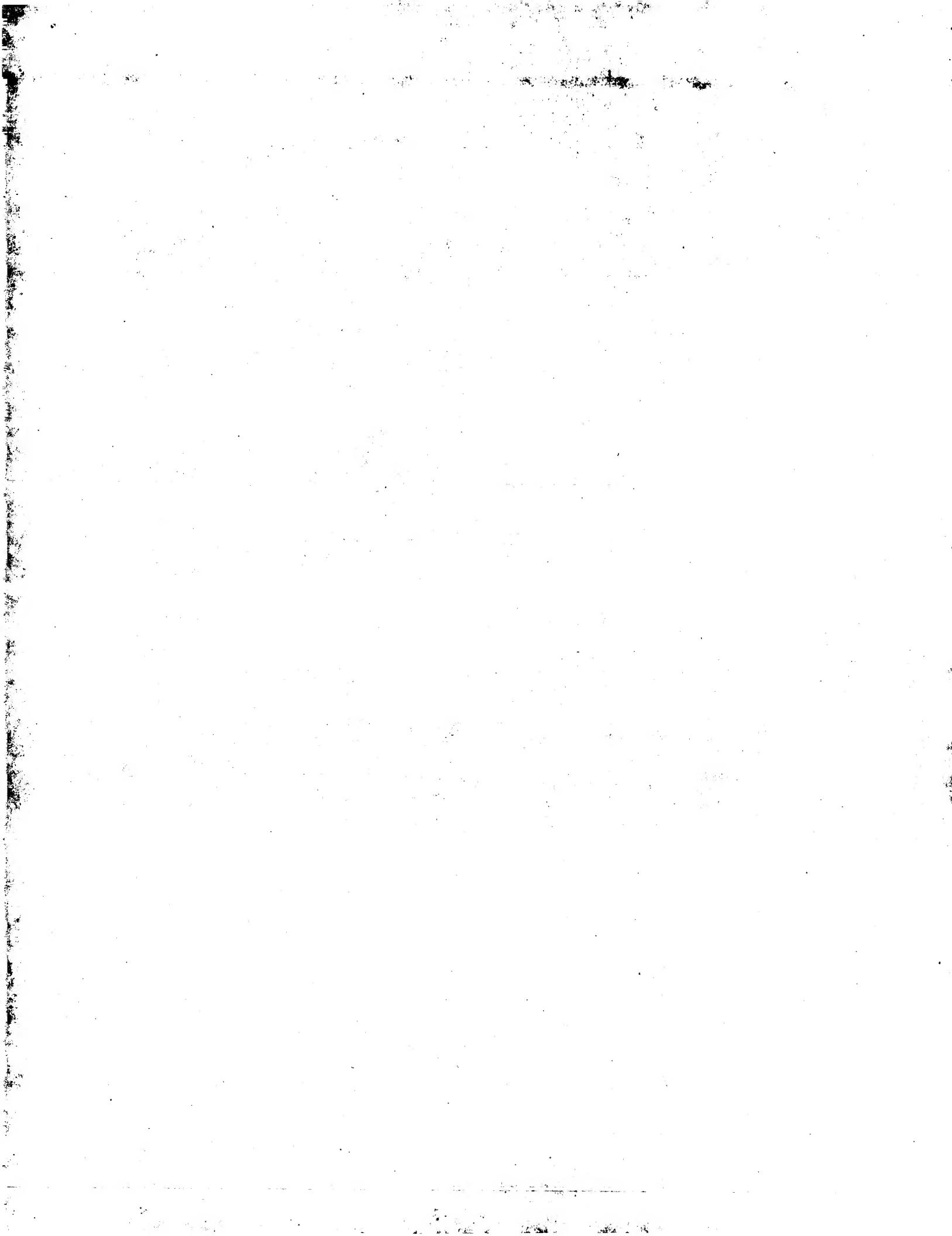
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2190 base pairs

; TYPE: nucleic acid

Search completed: May 22, 2003, 23:34:37
Job time : 66 secs



GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 22, 2003, 17:58:08 ; Search time 180 Seconds
 (Without alignments)
 1723.937 Million cell updates/sec

Title: US-09-847-102a-68

Perfect score: 1310
 Sequence: 1 MARPDAPPSSULLLAQL..... PNCAVPCYQPSFSADERTPA 235

Scoring table:

BLOSUM62 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODULE=frame+p2n.model -DEV=x1h
 -O= /cgn2_1/USPRT/spool/US09847102/runat_19052003_160412_844/app_query.fasta_1.391
 -DB=published_applications_NA -QFM=rnpb -MINMATCH=0.1
 -LOOCL=0 -LOOKEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
 -TRANS=human40_cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=per -THR MAX=100
 -THR MIN=0 -ALIGN=15 -MOB=LOCAL -OUTFM=pcto -NORM=ext -HEATSIZE=500 -MINLEN=0
 -MAXLEN=200000000 -USERID=US09847102 @CGN 1.1.57 @runat 19052003_160412_844
 -NCPU=6 -ICPU=3 -NO_MMW -LARGEQUERY=1 -NEGS=0 -WAIT -DSBLOCK=100
 -LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*

1: /cgn2_6/prodata/1/pubpna/us07_pubcomb.seq: *
 2: /cgn2_6/prodata/1/pubpna/pct NEW PUB.seq: *
 3: /cgn2_6/prodata/1/pubpna/us06_pubcomb.seq: *
 4: /cgn2_6/prodata/1/pubpna/us07_new_pub.seq: *
 5: /cgn2_6/prodata/1/pubpna/us07_NEW_PUB.seq: *
 6: /cgn2_6/prodata/1/pubpna/pctus_pubcomb.seq: *
 7: /cgn2_6/prodata/1/pubpna/us08_new_pub.seq: *
 8: /cgn2_6/prodata/1/pubpna/us08_pubcomb.seq: *
 9: /cgn2_6/prodata/1/pubpna/us09_new_pub.seq: *
 10: /cgn2_6/prodata/1/pubpna/us09_pubcomb.seq: *
 11: /cgn2_6/prodata/1/pubpna/us10_pubtomb.seq: *
 12: /cgn2_6/prodata/1/pubpna/us10_pubtomb.seq: *
 13: /cgn2_6/prodata/1/pubpna/us60_pubcomb.seq: *
 14: /cgn2_6/prodata/1/pubpna/us60_pubtomb.seq: *

ALIGNMENTS

RESULT 1
 US-10-152-548-9
 ; Sequence 9, Application US/10152548
 Publication No. US20030040051A1
 GENERAL INFORMATION:
 APPLICANT: Bhamot, Purrima
 Brink, Marcel
 Harryman, Cindy S.
 Wang, Yanshu
 Hsieh, Jen-chih
 Andrew, Deborah
 Nathans, Jeremy
 Nusse, Roeil
 NUMBER OF SEQUENCES: 18
 TITLE OF INVENTION: Wnt Receptor Compositions and Methods

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1310	100.0	2334 9 US-10-152-548-9	Sequence 9, Appli
2	823.5	62.9	2421 9 US-10-152-548-9	Sequence 15, Appli
3	754	57.6	424 10 US-09-867-01-6119	Sequence 6119, Appli
4	621	47.4	2344 9 US-10-152-548-1	Sequence 1, Appli

Alignment Scores:
 Pred. No.: 3.35e-72
 Score: 823.50
 Percent Similarity: 69.06%
 Best Local Similarity: 60.00%
 Query Match: 62.86%
 DB: 9

US-09-847-102a-68 (1-235) x US-10-152-548-15 (1-2421)

Qy 11 SerLeuIeu----leuLeuLeuLeuAlaGlnLeuValGlyArgAlaAlaAlaAlaLaser 28
 Db 218 TCGCTCCTAGCCGCCCTGGCGCTGGCGCTGGCGCTAGCGCTCTAGCGCGCTGGCC 277

Qy 29 LysAlaProValCysGlnGluIleThrValProMetCysArgGlyIleGlyTyrAlaLeu 48
 Db 278 AAGAGCGTGGCTGCCAGAGATCACCGTGCGCTGCCAGGCATGGTACACTAC 337

Qy 49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHis 68
 Db 338 ACTACATGCCAACCGTTCUACCAGAACAGAACAGTAGAGCGGGCTAGGGCAC 397

Qy 69 GlnPheIrrPProLeuValGluIleGlnCysSerProAspLeuArgGphePheLeuCysThr 88
 Db 398 CAGTTTGGCCGCTGGAGAATACAGTGCTCCCGGACCTCAAGTCTTCTGTGCTAGC 457

Qy 89 MetTYrThrProIleCysLeuProAspTYrHisLysProLeuProProCysArgSerVal 108
 Db 458 ATGTAACGCCATCTCCCTGAGGACTACAGAACCTCTCCGCTTGCGCTCTG 517

Qy 109 CysGluIargGlnAlaLysAlaGlyCysSerProLeuMetArgGlnTyrglyPheAlaTrpPro 128
 Db 518 TGTGANAGCGGCAGGGCTGGCGCCGGTCTATGCCGCACTACGGCTTGTGCTGCT 577

Qy 129 GluArgMetSerCysIapArgIeuProValLeuIArgAlaGluValLeuCysMet 148
 Db 578 GACCGCATGCGCTGCGATCGGTGCGGAGAGGGC---AACCGGAACTCTGTGCTAG 634

Qy 149 AspTYrAsnArgSerGluIalThrThrAla-----ProProArgProPheProAla 165
 Db 635 GACTACACCCACCCACCTCACACAGGCCGAGCCACCGGCCGCGCTGCTCCG 694

Qy 166 IlysProThrLeuProGly-----ProGly 174
 Db 695 CGCCCTCTC---CCGGGAGAGGCCGCCCCTGGAGGCCACAGCGCCGAGGG 751

Qy 175 Ala-----ProGly 175

Db 752 GCGAGCCCCACATCTGGCGCAGTAGGGCAGCCGGGAGCCGGGCTCGGCC 811

Qy 176 ProIlaSerGlyGlyGlucys-----ProIlaGlyGlyProPheVal----- 189

Db 812 CCTTCGCGCCGGGAAGGCCAGGCCCTGCGGGCTGCTCTGAGGGGG 871

Qy 190 CysLysCysBaaArgIluProPheAlaProIleIluGluUserHisProLeuTyraIlys 209
 Db 872 TCCCACTGCCGCCGCCATGCTGGCGCAGCGAACGCCACCGCTTACACCGC 931

RESULT 3

US-09-867-701-6119

; Sequence 6119 Application us/09867701

; Patent No. US20020132237A1

; GENERAL INFORMATION:

; APPLICANT: Aglate, Paul A.

; APPLICANT: Jones, Robert

US-09-847-102a-68 (1-235) x US-09-867-701-6119 (1-424)

ORGANISM: Homo sapien

US-09-867-701-6119

Alignment Scores:
 Pred. No.: 3.27e-66
 Score: 754.00
 Percent Similarity: 97.16%
 Best Local Similarity: 97.87%
 Query Match: 57.56%

Length: 424
 Matches: 137
 Conservative: 1
 Mismatches: 3
 Indels: 0
 Gaps: 0

US-09-847-102a-68 (1-235) x US-09-867-701-6119 (1-424)

Qy 33 CysGlnGluIleThrValProMetCysArgGlyIleGlyTyrAspLeuThrHistPro 52
 Db 2 TGCCAGGAATCACCGTGCCTGCGCATGTCGCGCGATCGCTACACTTGACGCC 61

Qy 53 AsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheIrrPro 72
 Db 62 AACCAAGTCACCAAGAACAGCAGGAGGAGGAGGAGGAGGCTGGAGGTCACCCATTCTCGGCC 121

Qy 73 LeuValGluIleGlnCysSerProLeuArgPhePheLeuCysThrMetTYrThrPro 92
 Db 122 CTGGGGAGATCCAATGCTCCGGACCTGGCTTCTCTATGCTCTACACGCC 181

Qy 93 IleCysIleProAspTYrHisLysProLeuProProCysArgSerValCysGluGala 112
 Db 182 ATCTGTCTGCCGCACTACACAGTCGCTGCGCCCTGCGCTCGTGTGGAGGC-GCC 240

Qy 113 LysAlaGlyCysSerProLeuMetArgGlnTyrglyPheAlaTrpProGluArgMetSer 132
 Db 241 AAGGCCGGCTCTCGCGCTGATGGCGCACTACGGCTTCGCTAGGCGCTAGGCG 300

Qy 133 CysAspArgIeuProValLeuIArgAspAlaGluValLeuCysMetAspTYrIasnArg 152
 Db 301 TCGGACGCCCTCCGGCTGGCCGAGGCCGAGGGCTCTGATGGATTACACCGC 360

Qy 153 SerGluIalThrAlaProProArgProPheProAlaLysProThrLeuProGlyPro 172
 Db 361 AGCGACGCCACACGCCGGCCCCAGGCCCTTCCAGCCAGCCACCCCTCCAGGCC 420

Qy 173 Pro 173

Db 421 CCA 423

RESULT 4

US-10-152-548-1

; Sequence 1, Application US/10152548

; Publication No. US20030040051A1

; GENERAL INFORMATION:

; APPLICANT: Bharat, Purvina
 Brink, Marcel
 Harryman, Cindy S.
 Wang, Yanshu
 Hasien, Jen-chih
 Andrew, Deborah
 Nathans, Jeremy
 Nusse, Roel

TITLE OF INVENTION: Wnt Receptor Compositions and Methods

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/152,348
 FILING DATE: 21-May-2002
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: US/08/832,340
 FILING DATE: 11-APR-1997
 APPLICATION NUMBER: US/60/015,307
 FILING DATE: 12-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 REFERENCE/DOCKET NUMBER: 8600-0167.30
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 234 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: b122 Polynucleotide, coding region
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-10-152-548-1
 Alignment Scores:
 Pred. No.: 3.34e-52
 Score: 621.00
 Percent Similarity: 55.80%
 Best local Similarity: 43.36%
 Query Match: 47.40%
 DB: 9
 DB: 1079 GACGAAAGGATTCGCC 1096
 RESULT 5
 US-10-152-548-1
 Sequence 13, Application US/10/152548
 Publication No. US2003040051A1
 GENERAL INFORMATION:
 APPLICANT: Bhanot, Purmina
 Brink, Marcel
 Harryman, Cindy S.
 Wang, Yanshu
 Hsieh, Jen-chih
 Andrew, Deborah
 Nathans, Jeremy
 Nusse, Roel
 TITLE OF INVENTION: Wnt Receptor Compositions and Methods
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/152,548
 FILING DATE: 21-May-2002
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/832,340
 FILING DATE: 11-APR-1997
 APPLICATION NUMBER: US 60/015,307

QY 73 LeuValGluIleGlnCysSerProSlePheArgPheLeuCvThrMetTyrThrPro 92
Db 1216 TTGGGAGGTGCACTGCTTCAGCCAGCTCAGTCAGTCCTTCAGTCGTCATCGCCCT 1275
QY 93 IleCysLeuProAspTyrHisLysProLeuProProCysArgSerValCysGluArgAla 112
Db 1276 GTGAGCACGCGTA---CTGGAGCAGCGCTCTGGCTCTGGCTCTGGAGGGGCC 1332
QY 113 LysAlaGlyCysSerProLeuMetArgLysGlyPheLeuLysProGluArgMetSer 132
Db 1333 CAG---GGTGCGAGCCACTCATGACAAGTCGCTTCAGTGCCAGACGGCTCAAG 1389
QY 133 CysSpargLeuProValLysGluArgAspAlaGluValLeuCysMetAspTyrSerArg 152
Db 1390 TGCGGAAAGTTCCTGTCACGGC-----GCAGAGAGCTGCGCTGGCCAGAAC 1443
QY 153 SerGluLysAlaThrAlaProProLysProProAlaLysProThrLeuProGlyPro 172
Db 1444 TCCGACAAGGCACCCGACTCCRCCTGCTGCCGAGCTGGACCAATCGCAG 1503
QY 173 ProGlyAlaProAlaSerGlyGlyGluCysProAlaGly-----Gly 186
Db 1504 CACGGGGGGGTACCGGGGCGTACCGGGAGGTGGCCGGGGGGAGGGGGGG 1563
QY 187 ProPheValCysLysCysArgGluProPheValProLeuLysGluSerHisProLeu 206
Db 1564 AAGTTCTCTGCGCC-----CGCGCCCTCAGGGTGCCTCCACTACTATCTG 1620
QY 207 TyrAsnLysValArgThrGlyGlnValProAsnCysAlaValProCysTyrGlnPro 226
Db 1621 GGGGAGAAG-----GACTCGGGCCCTGC---GAACCACT 1655
QY 227 -----PheserAlaAspGluArgThrPheAla 235
Db 1657 AAAGTATAACGGCTATGACTTCCGCCCTGAGGAATTGGCTTTCG 1704

RESULT 7
US-09-903-170C-10
; Sequence 10, Application US/09903170C
; Patent No. US20020156249A1
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M.
; APPLICANT: Bouwmeester, Tevis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; FILE REFERENCE: 51015-259
; CURRENT APPLICATION NUMBER: US/09/903,170C
; PRIORITY APPLICATION NUMBER: US 60/020,150
; PRIORITY FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 10
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Human FRZB-1
; US-09-903-170C-10

Alignment Scores:
Pred. No.: 2.71e-28 Length: 1893
Score: 378.00 Matches: 84
Percent Similarity: 49.79% Conservative: 34
Best Local Similarity: 35.44% Mismatches: 83
Query Match: 28.85% Indels: 36
DB: 9 Gaps: 8

US-09-847-102A-68 (1-235) x US-09-903-170C-10 (1-1893)
; Sequence 4, ProAspProSerAla-----ProProSerLeuLeuLeuLeuLeuLeu 17
; DB: 40 CCTGCCCACTCTGGGGATCATGGCTCTGGGGACCCGGAGGGATGCTGCTGGG 99
; 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerLysAlaPro 31

RESULT 7
US-09-903-170C-10
; Sequence 10, Application US/09903170C
; Patent No. US20020156249A1
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M.
; APPLICANT: Bouwmeester, Tevis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; FILE REFERENCE: 51015-259
; CURRENT APPLICATION NUMBER: US/09/903,180B
; PRIORITY APPLICATION NUMBER: US 60/020,150
; PRIORITY FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 10
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Human FRZB-1
; US-09-903-180B-10

Alignment Scores:
Pred. No.: 2.71e-28 Length: 1893
Score: 378.00 Matches: 84
Percent Similarity: 49.79% Conservative: 34
Best Local Similarity: 35.44% Mismatches: 83
Query Match: 28.85% Indels: 36
DB: 9 Gaps: 8

US-09-847-102A-68 (1-235) x US-09-903-170C-10 (1-1893)
; Sequence 4, ProAspProSerAla-----ProProSerLeuLeuLeuLeuLeuLeu 17
; DB: 40 CCTGCCCACTCTGGGGATCATGGCTCTGGGGACCCGGAGGGATGCTGCTGGG 99
; 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerLysAlaPro 31

QY 100 GGCGGGTCCCCCGCCCGCCCTCTCTCTCTCGCTCGCGGCGGCGGCGCTCGGGCTCA 159
Db 32 ValCysGlnGluIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrMet 51
QY 160 GCGTGTAGCCGCTCCCATCCCTCTCTGCAAGTCGCTCTGGAACTGACTAAGTG 219
QY 52 ProAspGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrp 71
Db 220 CCCAACCCACTGCACTCAGACTCAGGCCAACGCCATCTCGCCATCGAGTCGAA 279
QY 72 ProLeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetTyrThr 91
Db 340 CCACATCGCACCATGACTTCAGCACGAGCCATCACGCCCTGTAAGTCGCTGCGAG 399
QY 280 GGTCTGGGACCACTGAGCCGATCTGCTCTCTCTCTGCGCATGACCG 339
QY 92 ProLeuCysIleProAspTyr---HisLysProLeuProProCysArgSerValCysGlu 110
Db 340 CCACATCGCACCATGACTTCAGCACGAGCCATCACGCCCTGTAAGTCGCTGCGAG 399
QY 111 ArgAlaLysAlaGlyCysSerProLeuMetArgLysGlyPheAlaProTyrGluArg 130
Db 400 CGGCGGGCGAGGCTGAGCCCATACTCTCAAGTACGCCACTGTGGCCGGAGAC 459
QY 131 MetSerCysSpargLeuProValLysGluArgAspAlaGluValLeuCysMetAspTyr 150
Db 460 CTGGCTCGGGAGGCTGAGCCAGGAGG-----GTCGTC 504
QY 151 AspArgSerGluLysAlaThrAlaProProLysProThrLeuPro 170
Db 505 TCTCCGAGGCGATCGTCACTCGGGAGGACTGTGATTTCT----- 546
QY 171 GlyProProGlyAlaProAlaSerGlyGlyGlyCysProAlaGlyGlyProLeu 190
Db 547 -----ATGGATTCTGACTGACGGAAGCTGTAGAGGGCAGCAGGAAACGGCTGT 594
QY 191 LysCysArgGluProPheValProLeuLysGluSerHisProLeu----- 206
Db 595 AAATGTTAG-----CTTATTAGACTACAGAGAACCTTCCGGAACAT 642
QY 207 TyrAsnLysValArgThrGlyGlnValProAsnCysAlaValProCysTyr 223
Db 643 TACAATCTATGTCATTGGCTAACGTTAAAGGATAAAGACTAAGTGGCCAT 693

RESULT 8
US-09-903-180B-10
; Sequence 10, Application US/09903180B
; Patent No. US20020099171A1
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M.
; APPLICANT: Bouwmeester, Tevis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; FILE REFERENCE: 51015-256
; CURRENT APPLICATION NUMBER: US/09/903,180B
; PRIORITY APPLICATION NUMBER: US 60/020,150
; PRIORITY FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 10
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Human FRZB-1
; US-09-903-180B-10

Alignment Scores:
Pred. No.: 2.71e-28 Length: 1893
Score: 378.00 Matches: 84
Percent Similarity: 49.79% Conservative: 34
Best Local Similarity: 35.44% Mismatches: 83
Query Match: 28.85% Indels: 36
DB: 9 Gaps: 8

US-09-847-102a-68 (1-235) x US-09-903-180B-10 (1-1893)

QY 4 ProAspProSerAla-----ProProSerLeuleuleuleuleu 17
Db 40 CCTGCCCATCTGGGATCATGGTGTGGCAGCCGGAGGGATCTCTGCCTGG 99
QY 18 AlaGlnIeuValGlyArgAlaAla-----AlaIaSerIysAlaPro 31
Db 100 GCGGGCTCTTCCCTGGCTGCTCTGCCCTCGGGGCCGGGCTGGGCTGCA 159
QY 32 ValCysGlnGluIleThrValProMetCysArgGlyIleGlyTyraLeuThrIleMet 51
Db 160 GCTGTGAGCCCCGTCGCATCCCTCTGCAAGTCTCCCTGCCCTGGAACTACTAAGATG 219
QY 52 ProAspGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrp 71
Db 220 CCAAACACCCTGACCACAGCACTCAGGCCAACGCCATCCCTGCCATGAGCTGAA 279
QY 72 ProLeuValGluIleGlyCysSerProAspLeuArgphepheLeuCysThrMetTyrThr 91
Db 280 GCTCTGCTGGCACCACTGAGCCATCTGCAGCCGATCTCTCTCTCTCTGCTGCA 339
QY 92 ProLeuValProAspTyr---HisLysProLeuProProCysArgSerValCysGlu 110
Db 340 CCCATCTGCACTTGTACTTCCAGCACAGCCATCAAGCCCTGTAAGTCTCTGCTGGAG 399
QY 111 ArgAlaLysValGlyCysSerProLeuMetArgGlnTyrglyPheAlaIaTrpProGluArg 130
Db 400 CGGGCCGGCAGGGCTGTGACCCACTCTGCAACGCGCACTCTGCGCCATCTGAGCTGCA 459
QY 131 MetSerCysAspArgLeuProValLeuGluValuCysMetAspTyr 150
Db 460 CTGGCTCTGGGACCCCACCTGAGCCATCTCTCAAGTACGACGCGACTCTGCGCCATGAGCTGCA 504
QY 151 AsnArgSerGluAlaThrAlaProProArgProheProAlaLysProThrLeuPro 170
Db 505 TCTCCGAGGCCATCTGGACGGAGCTGTATTCT----- 546
QY 171 GlyProProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyGlyProheValCys 190
Db 547 -----ATGGATTCTGTAAGGAACACTGTAGAGGAGGCAAGCAGTGAACTGT 594
QY 191 LysCysArgGluProheValProleLeuLysGluSerHisProLeu----- 206
Db 595 AAATGTAAG-----CTTATAGAGCTACAGAGACCTATTCCGGAAACAT 642
QY 207 TyrAsnLysValArgGlyGlyGlyGlyValProAsnCysAlaValProCysTyr 223
Db 643 TACAACATATGTCATTGGGCTAAAGTTAAAGAGATAAAAGACTAAGTGCCAT 693

RESULT 9
US-09-903-187A-10
; Sequence 10, Application US/09903187A
; Patent No. US20020099172A1
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M.
; APPLICANT: Bouwmeester, Tevis B
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; FILE REFERENCE: 510015-248
; CURRENT APPLICATION NUMBER: US/09/903, 187A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/552, 988
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: US 08/878, 474
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: US 60/020, 150
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 1893
; TYPE: DNA

i ORGANISM: Human
US-09-903-187A-10
Alignment Scores: 2.71e-28 Length: 1893
Pred. No.: 378.00 Matches: 84
Score: 49.79% Conservative: 34
Percent Similarity: 35.44% Mismatches: 83
Best Local Similarity: 28.85% Index: 36
Query Match: 10 Gaps: 8
DB:

US-09-847-102a-68 (1-235) x US-09-903-187A-10 (1-1893)

QY 4 ProAspProSerAla-----ProProSerLeuleuleuleu 17
Db 40 CCTGCCCATCTGGGATCATGGTGTGGCAGCCGGAGGGATCTCTGCCTGG 99
QY 18 AlaGlnIeuValGlyArgAlaAla-----AlaIaSerIysAlaPro 31
Db 100 GCGGGCTCTTCCCTGGCTGCTCTGCCCTCGGGGCCGGGCTGGGCTGCA 159
QY 32 ValCysGlnGluIleThrValProMetCysArgGlyIleGlyTyraLeuThrIleMet 51
Db 160 GCTGTGAGCCCCGTCGCATCCCTCTGCAAGTCTCCCTGCCCTGGAACTACTAAGATG 219
QY 52 ProAspGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrp 71
Db 220 CCAAACACCCTGACCACAGCACTCTGCAACGCGCACTCTGCGCCATCTGAGCTGCA 279
QY 18 AlaGlnIeuValGlyArgAlaAla-----AlaIaSerIysAlaPro 31
Db 100 GCGGGCTCTTCCCTGGCTGCTCTGCCCTCGGGGCCGGGCTGGGCTGCA 159
QY 32 ValCysGlnGluIleThrValProMetCysArgGlyIleGlyTyraLeuThrIleMet 51
Db 160 GCTGTGAGCCCCGTCGCATCCCTCTGCAAGTCTCCCTGCCCTGGAACTACTAAGATG 219
QY 52 ProAspGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrp 71
Db 220 CCAAACACCCTGACCACAGCACTCTGCAACGCGCACTCTGCGCCATCTGAGCTGCA 279
QY 72 ProLeuValGluIleGlyCysSerProAspLeuArgphepheLeuCysThrMetTyrThr 91
Db 280 GCTCTGCTGGGACCCCACCTGAGCCATCTCCCTGCGCTGCTCTCTGCGCTGCA 339
QY 92 ProLeuValProAspTyr---HisLysProLeuProProCysArgSerValCysGlu 110
Db 340 CCCATCTGCACTTGTACTTCCAGCACAGCCATCAAGCCCTGTAAGTCTCTGCTGGAG 399
QY 111 ArgAlaLysValGlyCysSerProLeuMetArgGlnTyrglyPheAlaIaTrpProGluArg 130
Db 400 CGGGCCGGCAGGGCTGTGACCCACTCTGCAACGCGCACTCTGCGCCATCTGAGCTGCA 459
QY 131 MetSerCysAspArgLeuProValLeuGluValuCysMetAspTyr 150
Db 460 CTGGCTCTGGGACCCCACCTGAGCCATCTCTCAAGTACGACGCGACTCTGCGCCATGAGCTGCA 504
QY 151 AsnArgSerGluAlaThrAlaProProArgProheProAlaLysProThrLeuPro 170
Db 505 TCTCCGAGGCCATCTGGACGGAGCTGTATTCT----- 546
QY 171 GlyProProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyGlyProheValCys 190
Db 547 -----ATGGATTCTGTAAGGAACACTGTAGAGGAGGCAAGCAGTGAACTGT 594
QY 191 LysCysArgGluProheValProleLeuLysGluSerHisProLeu----- 206
Db 595 AAATGTAAG-----CTTATAGAGCTACAGAGACCTATTCCGGAAACAT 642
QY 207 TyrAsnLysValArgGlyGlyGlyGlyValProAsnCysAlaValProCysTyr 223
Db 643 TACAACATATGTCATTGGGCTAAAGTTAAAGAGATAAAAGACTAAGTGCCAT 693

RESULT 10
US-09-903-171A-10
; Sequence 10, Application US/09903171A
; Patent No. US2002123613A1
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M.
; APPLICANT: Bouwmeester, Tevis B
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; FILE REFERENCE: 510015-250
; CURRENT APPLICATION NUMBER: US/09/903, 171A
; CURRENT FILING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: US 60/020,150
; PRIORITY FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 10
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Human FRZB-1
; US-09-903-171A-10

Alignment Scores:
Pred. No.: 2.71e-28 Length: 1893
Score: 378.00 Matches: 84
Percent Similarity: 49.79% Conservative: 34
Best Local Similarity: 35.44% Mismatches: 83
Query Match: 28.85% Indels: 36
DB: 10 Gaps: 8

US-09-847-102A-68 (1-235) x US-09-903-171A-10 (1-1893)
Qy 4 ProAspProSerAla-----J-ProProSerLeuLeuLeuLeuLeu 17
Db 40 CCTGCCCATCTCGGGATCATGGTCCTGGGAGCCGGAGGGATCTGTGCTGG 99
Qy 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerLysAlaPro 31
100 GcCGGCGCTTGCCTGGCTGGCTCTGGCTGGCTGGCTGGCTGGCGCA 159
Qy 32 ValCysGlnGluLeuThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMet 51
Db 160 GCTGTGAGCCGTCGCATCCCTGTCAGTCCTGGCTGGAACTGACTAAGTG 219
Qy 52 ProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrp 71
Db 220 CCCAACACCTGGACCACAGCACTGAGCCAAAGCCATCTGGCCATRGAGGAGTCAA 279
Qy 72 ProLeuValGluIleGlyCysSerProAspLeuArgPheLeuCysThrMetTyrThr 91
Db 280 GGTCGTGCGGGCACCTGAGCCCCATCTGCTCTGCGCAGTGAGCG 339
Qy 92 ProLeuCysLeuProAspTyr--HisLysProLeuProProCysArgSerValCysGlu 110
Db 340 CCCATCTGACCACTTGAATTCCAGCACGCCATCAAGCCCTGTAAGTCTGTGAG 399
Qy 111 ArgAlaLysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArg 130
Db 400 CGGCCCCGGCAGGCTGTGAGCCATACTCTCAAGTACGCCACTCTGGCCGAGAAC 459
Qy 131 MetSerCysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyr 150
Db 460 CTGCCTGGAGGAGCTGCCAGTGTACACAGGGC-----GTTGCACTC----- 504
Qy 151 AsnArgSerGluAlaThrAlaProProArgProPheProAlaLysProThrLeuPro 170
Db 505 TCTCCGAGGCCATCGTTACTGGGACGGAGCTGATTCCT----- 546
Qy 171 GlyProProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyGlyProHeValCys 190
Db 547 -----ATGGATCTACTAACGAACTGTGAGGGCAAGCAGTGACCGCTGT 594
Qy 191 LysCysArgGluProPheValProAlaLeuLysGluSerHisProLeu----- 206
Db 595 AAATGTTAG-----CTTATGAGCTACACAGAAGACCTATTCCGGAAACAT 642
Qy 207 TyrAspLysValArgThrGlyGlnValProAsnCysAlaValProCysTyr 223
Db 643 TACACTATGTCATCGGGCTAAAGTAAAGAGATAAGACTAAGTAGTCCAT 693

RESULT 11
US-09-903-188A-10
; Sequence 10, Application us/09903188A
; Patent No. US2002128439A1
; GENERAL INFORMATION:

APPLICANT: De Robertis, Edward M.
; APPLICANT: Bouwmeester, Tevis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; TITLE OF INVENTION: Factors
; FILE REFERENCE: S10015-258
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/020,150
; PRIOR FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 10
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Human FRZB-1
; US-09-903-188A-10

Alignment Scores:
Pred. No.: 2.71e-28 Length: 1893
Score: 378.00 Matches: 84
Percent Similarity: 49.79% Conservative: 34
Best Local Similarity: 35.44% Mismatches: 83
Query Match: 28.85% Indels: 36
DB: 10 Gaps: 8

US-09-847-102A-68 (1-235) x US-09-903-188A-10 (1-1893)
Qy 4 ProAspProSerAla-----J-ProProSerLeuLeuLeuLeuLeu 17
Db 40 CCTGCCCATCTCGGGATCATGGTCCTGGGAGCCGGAGGGATCTGTGCTGG 99
Qy 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerLysAlaPro 31
100 GcCGGCGCTTGCCTGGCTGGCTCTGGCTGGCTGGCTGGCGCA 159
Qy 32 ValCysGlnGluLeuThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMet 51
Db 160 GCTGTGAGCCGTCGCATCCCTGTCAGTCCTGGCTGGAACTGACTAAGTG 219
Qy 52 ProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrp 71
Db 220 CCCAACACCTGGACCACAGCACTGAGCCAAAGCCATCTGGCCATRGAGGAGTCAA 279
Qy 72 ProLeuValGluIleGlyCysSerProAspLeuArgPheLeuCysThrMetTyrThr 91
Db 160 GGTCGTGCGGGCACCTGAGCCCCATCTGCTCTGCGCAGTGAGCG 339
Qy 52 ProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrp 71
Db 220 CCCAACACCTGGACCACAGCACTGAGCCAAAGCCATCTGGCCATRGAGGAGTCAA 279
Qy 72 ProLeuValGluIleGlyCysSerProAspLeuArgPheLeuCysThrMetTyrThr 91
Db 280 GGTCGTGCGGGCACCTGAGCCCCATCTGCTCTGCGCAGTGAGCG 339
Qy 92 ProLeuCysLeuProAspTyr--HisLysProLeuProProCysArgSerValCysGlu 110
Db 340 CCCATCTGACCACTTGAATTCCAGCACGCCATCAAGCCCTGTAAGTCTGTGAG 399
Qy 111 ArgAlaLysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArg 130
Db 400 CGGCCCCGGCAGGCTGTGAGCCATACTCTCAAGTACGCCACTCTGGCCGAGAAC 459
Qy 131 MetSerCysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyr 150
Db 340 CCCATCTGACCACTTGAATTCCAGCACGCCATCAAGCCCTGTAAGTCTGTGAG 399
Qy 92 ProLeuCysLeuProAspTyr--HisLysProLeuProProCysArgSerValCysGlu 110
Db 400 CGGCCCCGGCAGGCTGTGAGCCATACTCTCAAGTACGCCACTCTGGCCGAGAAC 459
Qy 131 MetSerCysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyr 150
Db 460 CTGGCCCTGGAGGAGCTGCCAGTGTGAGCAGGGC-----GTTGCACTC----- 504
Qy 111 ArgAlaLysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArg 130
Db 400 CGGCCCCGGCAGGCTGTGAGCCATACTCTCAAGTACGCCACTCTGGCCGAGAAC 459
Qy 131 MetSerCysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyr 150
Db 505 TCTCCGAGGCCATCGTTACTGGGACGGAGCTGATTCCT----- 546
Qy 171 GlyProProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyGlyProHeValCys 190
Db 547 -----ATGGATCTACTAACGAACTGTGAGGGCAAGCAGTGACCGCTGT 594
Qy 151 AsnArgSerGluAlaThrAlaProProArgProPheProAlaLysProThrLeuPro 170
Db ::----- 546
Qy 131 MetSerCysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyr 150
Db 505 TCTCCGAGGCCATCGTTACTGGGACGGAGCTGATTCCT----- 546
Qy 171 GlyProProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyGlyProHeValCys 190
Qy 151 AsnArgSerGluAlaThrAlaProProArgProPheProAlaLysProThrLeuPro 170
Db 547 -----ATGGATCTACTAACGAACTGTGAGGGCAAGCAGTGACCGCTGT 594
Qy 191 LysCysArgGluProPheValProAlaLeuLysGluSerHisProLeu----- 206
Db 595 AAATGTTAG-----CTTATGAGCTACACAGAAGACCTATTCCGGAAACAT 642
Qy 207 TyrAspLysValArgThrGlyGlnValProAsnCysAlaValProCysTyr 223

Db 643 TACAACTATGTCATTGGGCTAAGTTAACAGATAAAGACTAAGTGCAT 693
 RESULT 12
 US-09-903-323A-10
 ; Sequence 10, Application US/09903323A
 ; Patent No. US20020128410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: De Robertis, Edward M.
 ; BOWMEISTER, Lewis
 ; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
 ; FILE REFERENCE: 510015-261
 ; CURRENT APPLICATION NUMBER: US/09/903,323A
 ; CURRENT FILING DATE: 2001-07-11
 ; PRIOR APPLICATION NUMBER: US 60/020,150
 ; PRIOR FILING DATE: 1996-06-20
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO: 10
 ; LENGTH: 1893
 ; TYPE: DNA
 ; ORGANISM: Human PRZB-1
 ; US-09-903-323A-10
 Alignment Scores:
 Pred. No.: 2.71e-28 Length: 1893
 Score: 378.00 Matches: 84
 Percent Similarity: 49.79% Conservative: 34
 Best Local Similarity: 35.44% Mismatches: 83
 Query Match: 28.85% Indexes: 36
 DB: 10 Gaps: 8
 US-09-847-102A-68 (1-235) x US-09-903-323A-10 (1-1893)
 Qy 4 ProAspProSerAla-----ProProSerLeuLeuLeuLeuLeuLeu 17
 Db 40 CCTGCCCATCTGCCGGATCATGGTGTGGGCAASCCCGGAGGGATGCTGCTGCGG 99
 Qy 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerLysAlaPro 31
 Db 100 GCGGCGCTGCTGCTGCCCTGGCTCTCTGCCCTGCCCTGCCGCCGCTGCCGCTGCA 159
 Qy 32 ValCysGlnGluLysLeuProMetCysArgGlyIleGlyTyrosLeuThrHisMet 51
 Db 160 GCCTGTGAGGCCGTCGCCATCCCCCTGCKAGTCCTGCTGCCATCGACAGCTGAA 219
 Qy 52 ProAlaGlnPheAsnHiSASPThrGlnAspGluAlaGlyLeuGluValHiGlnHetrp 71
 Db 220 CCCAACACCCTGACCAAGACTCAGGCCATCCGGCATCGACAGCTGAA 279
 Qy 72 ProLeuValGluLysLeuGlnCysSerProAspLeuArgPheLeuCystHMeTyrThr 91
 Db 280 GGTCCTCTGCGCACCACTGCGGCCGATCTGCCCTCTCTCTGCGCATGACGG 339
 Qy 92 ProLeuCysLeuProAspTyr--HisLysProLeuProProCysArgSerValCysGlu 110
 Db 340 CCGATCTGCACCACTGACTTCAGCAAGGCCATCAAGCCCTGCTGTCGAG 399
 Qy 111 ArgAlaLysAlaLysGlyCysSerProLeuMetArgGlnTrpGlyPheAlaTrpProGluArg 130
 Db 400 CGGGCCGGCGAGGGCTGAGCCCATACTCTCAAGTACGCCACTCTGGCCGAGAAC 459
 Qy 151 AsnArgSerGluAlaLysThrAlaProProArgProPheProAlaLysProThrLeuPro 170
 Db 505 TCTCCGAGGGCATCTTACTCCGGACGGAGCTGATTTCTC 504
 Qy 171 GlyProProGlyAlaProAlaSerGlyGlyValCysProAlaLysGlyProPheValCys 190
 Db 547 -ATGGATCTAGTAACGGAACACTGTAGAGGGCAAGCAGTGACGCTGT 594
 Qy 191 LysCysBarglLysProPheAlaProLeuLysGluSerHiProLeu----- 206
 Db 595 AAATGAA-----CCATTAGCTACAGAGACCTATTCGGGACAAAT 642
 Qy 207 TYRAspLysValArgThrGlyGlnValProAlaCysAlaValProCysTyr 223
 Db 643 TACAACTATGTCATTGGGCTAAGTTAACAGATAAAGACTAAGTGCAT 693
 RESULT 13
 US-09-903-325A-10
 ; Sequence 10, Application US/09903325A
 ; Patent No. US20020128410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: De Robertis, Edward M.
 ; BOWMEISTER, Lewis
 ; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
 ; FILE REFERENCE: 510015-257
 ; CURRENT APPLICATION NUMBER: US/09/903,325A
 ; CURRENT FILING DATE: 2001-11-07
 ; PRIOR APPLICATION NUMBER: US 60/020,150
 ; PRIOR FILING DATE: 1996-06-20
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO: 10
 ; LENGTH: 1893
 ; TYPE: DNA
 ; ORGANISM: Human PRZB-1
 ; US-09-903-325A-10
 Alignment Scores:
 Pred. No.: 2.71e-28 Length: 1893
 Score: 378.00 Matches: 84
 Percent Similarity: 49.79% Conservative: 34
 Best Local Similarity: 35.44% Mismatches: 83
 Query Match: 28.85% Indexes: 36
 DB: 10 Gaps: 8
 US-09-847-102A-68 (1-235) x US-09-903-325A-10 (1-1893)
 Qy 4 ProAspProSerAla-----ProProSerLeuLeuLeuLeuLeuLeu 17
 Db 40 CCTGCCCATCTGCCGGATCATGGTGTGGGCAASCCCGGAGGGATGCTGCTGCGG 99
 Qy 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerLysAlaPro 31
 Db 100 GCGGCGCTGCTGCTGCCCTGGCTCTCTGCCCTGCCCTGCCGCCGCTGCCGCTGCA 159
 Qy 32 ValCysGlnGluLysLeuProMetCysArgGlyIleGlyTyrosLeuThrHisMet 51
 Db 160 GCCTGTGAGGCCGTCGCCATCCCCCTGCKAGTCCTGCTGCCATCGACAGCTGAA 219
 Qy 52 ProAlaGlnPheAsnHiSASPThrGlnAspGluAlaGlyLeuGluValHiGlnHetrp 71
 Db 220 CCCAACACCCTGACCAAGACTCAGGCCATCCGGCATCGACAGCTGAA 279
 Qy 72 ProLeuValGluLysLeuGlnCysSerProAspLeuArgPheLeuCystHMeTyrThr 91
 Db 280 GGTCCTCTGCGCACCACTGCGGCCGATCTGCCCTCTCTGCGCATGACGG 339
 Qy 92 ProLeuCysLeuProAspTyr--HisLysProLeuProProCysArgSerValCysGlu 110
 Db 340 CCGATCTGCACCACTGACTTCAGCAAGGCCATCAAGCCCTGCTGTCGAG 399
 Qy 111 ArgAlaLysAlaLysGlyCysSerProLeuMetArgGlnTrpGlyPheAlaTrpProGluArg 130
 Db 400 CGGGCCGGCGAGGGCTGAGCCCATACTCTCAAGTACGCCACTCTGGCCGAGAAC 459
 Qy 131 MetSerCysBarglLysProValLeuGlyArgAspAlaGluValLeuCysMetAspTyr 150
 Db 460 CTGGCTCTGCGAGGAGCTGCGCTGCTGACGACGGGGC-----GTCGACATC 504
 Qy 151 AsnArgSerGluAlaLysThrAlaProProArgProPheProAlaLysProThrLeuPro 170
 Db 505 TCTCCGAGGGCATCTTACTCCGGACGGAGCTGATTTCTC 504
 Qy 171 GlyProProGlyAlaProAlaSerGlyGlyValCysProAlaLysGlyProPheValCys 190
 Db 460 CTGGCTCTGCGAGGAGCTGCGCTGACGACGGGGC-----GTCGACATC 504

Search completed: May 22, 2003, 21:14:02
Job time : 188 SECs

Job time : 188 sec



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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 22, 2003, 19:43:08 ; Search time 1516 Seconds
(Without alignments)
2510.514 Million cell updates/sec

Title: US-09-847-102a-68
Perfect score: 1310
Sequence: 1 MARPDPSAPPSTLLLQL.....PNCAVPCYQPSFSADERTFA 235

Scoring table: BL0SUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
DelOp	6.0	Delect	7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32208132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-MODEL=frame+p2n.model -DEV=x1h
-Q=cgn_1_usp0_spool/US09847102/runat_19052003_160405_735/app_query.fasta_1.391
-DB_BST -QFMT=fastap -SUFFIX=est -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIXX=blosum62 -TRANS=human40_cdi -LIST=45
-DOCFILE=200 -THR SCOREPCC -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORMEXT -HMAPSIZE=500 -MINLEN=0 -MAXLEN=00000000
-USER=US09847102 @CGN 1_1 1905 @runat_19052003_160406_736 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NE=0 -SORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAROP=10 -XGAPEXT=0.5 -FGAROP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : EST.*

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2: em_eethum:*	c	401.5	30.6	934	14	BQ651465
3: em_eetcin:*	c	399	30.5	935	9	A1794418
4: em_eetcmu:*	c	399	30.4	949	9	AA107737
5: em_eetcov:*	c	397.5	30.3	918	14	BW97842
6: em_eetcpl:*	c	396.5	30.3	918	14	BQ650644
7: em_eetcro:*	c	394.5	30.1	857	14	BQ650917
8: em_eetcrc:*	c	394.5	30.1	1086	14	BW97842
9: gb_eetc1:*	c	394.5	30.1	1086	14	BQ650917
10: gb_eetc2:*	c	394.5	30.1	1086	14	BW97842
11: gb_eetc:*	c	386.5	29.5	360	14	C49875
12: gb_eetc3:*	c	386.5	29.5	360	14	BQ65492
13: gb_eetc4:*	c	383.5	29.3	1317	14	BQ65492
14: gb_eetc5:*	c	382.5	29.2	1030	14	BQ647904
15: em_eetcfun:*	c	381.5	29.2	213	9	AK021164
16: em_eatom:*	c	381.5	29.1	360	9	AK021164
17: gb_gbs:*	c	381.5	29.1	360	14	C3986
18: em_gbs_hum:*	c	381.5	29.1	891	17	CNS0434
19: em_gbs_inv:*	c	381.5	29.1	417	9	A1543106
20: em_gbs_pin:*	c	379.5	29.0	417	9	A1543106
21: em_gbs_vrt:*	c	379.5	28.9	1083	14	BQ53826
22: em_gbs_fun:*	c	376.5	28.8	610	13	B155656
23: em_gbs_mam:*	c	376.5	28.7	376	14	C39238
24: em_gbs_mus:*	c	376.5	28.7	376	14	C39238
25: em_gbs_other:*	c	376.5	28.7	376	14	C39238
26: em_gbs_pro:*	c	376.5	28.7	376	14	C39238
27: em_gbs_rnd:*	c	376.5	28.7	376	14	C39238

RESULTS

ALIGNMENTS

RESULT 1
BE953717

LOCUS BB953717 DEFINITION UI-M-CCL-azz-c-04-0-UI_81 NIH_BMAP_Reti_N Mus musculus cDNA clone ACCESSION BB953717 VERSION BE953717.1 GI:10595515 KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 492)
AUTHORS Bonaldo,M.F., Leinon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene

Best Local Similarity: 97.16% Mismatches: 3
 Query Match: 57.56% Indels: 1
 DB: 9 Gaps: 0

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 /db_xref="taxon:98883"
 /clone="83G18"
 /clone_lib="G"
 /note="Genoscope sequence ID : COAG183BD091P1-end : T7"

US-09-847-102A-68 (1-235) x AA481448 (1-424)

QY 33 CysGlnGluIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
 2 ProCCAGGAATACGGTGCCATGCGCCGCATCGCTACACCTGACCCATGCCC 61
 QY 53 AsnGlnPheAsnHisAspThrGlnAspGluLalaGluLeuGluValHisGlnPheTrpPro 72
 62 AACAGAGTCAAACCACGACACCCAGGAGGAGGGGCTGGGGTGACCAAGTCGCCG 121
 Db 73 LeuValGluIleGlnCysSerProAspLeuIrgPheAspLeuLysCysThrMetYrrThrPro 92
 122 CTGGTGGAGGAGCCAATCTCCGCGAACCTGCGCTTCCTCATGCTCTATCACGCC 181
 QY 93 IleCysLeuProAspThrIlysProLeuProProCysArgSerValCysGluArgAla 112
 182 ARCTGTTGTCGCCGACTACACAGTCGCTGCCCTCGGAGTGCGAGGC-GCC 240
 QY 113 LysAlaIgLyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArgMetSer 132
 241 AAGGCCGGCTCTCGCGCTATGCCAGTACGGGCTCGCTAGGCCGAGCGATGAGC 300
 QY 133 CysAspArgLysProValLeuGlyArgAspGluAlaGluValLeuCysMetAspTyrAsnArg 152
 301 TCGGACGCCCTCCGGCTGCTGGCCGGACCCGAGCTCCCTGCGATGGATACACGC 360
 QY 153 SerGluLysThrAlaProProArgProHeProlAlaLysProThrLeuProGlyPro 172
 361 AGCGAGGCCAACCGGCCGCCAGGCCTTCCAGCCAAAGCCCACCCCTTCAGGCCG 420
 QY 173 Pro 173
 Db 421 CCA 423

RESULT 3
 CNS02ZUH
 DEFINITION Cns02Zuh
 LOCUS Tetraodon nigroviridis 1028 bp DNA linear GSS 15-MAY-2000
 VERSION AL221426.1 GI:7880245
 KEYWORDS GSS; genome survey sequence.
 SOURCE Tetraodon nigroviridis.
 ORGANISM Tetraodon nigroviridis
 AUTHORS Eukayora; Matzosa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
 1 (bases 1 to 1028)
 Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
 TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1028)
 AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
 TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1028)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2000)
 COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis

genome. For more information, please take a look at
<http://www.genoscope.cnrs.fr/Tetraodon>.

FEATURES
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 /db_xref="taxon:98883"
 /clone="183G18"
 /clone_lib="G"
 /note="Genoscope sequence ID : COAG183BD091P1-end : T7"
 BASE COUNT 143 a 393 c 301 g 185 t 6 other_B
 ORIGIN ORIGIN
 Alignment Scores:
 Pred. No.: 2.98e-44 Length: 1028
 Score: 653.50 Matches: 129
 Percent Similarity: 68.57% Conservative: 15
 Best Local Similarity: 61.43%
 Query Match: 49.89% MisMatches: 44
 DB: 17 Gaps: 23
 US-09-847-102A-68 (1-235) x CNS02ZUH (1-1028)

QY 37 ThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsn 56
 Db 1 ACGGTCCCCATGGCAGGACATCGCTACACCTACATGCCAACCGAGTCAC 60
 QY 57 HisAspPThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGluIle 76
 Db 61 CACGAGACCCAGGAGGAGGAGGCTGAGGTGACCCAGTCTGGCCCTGTGCGTATC 120
 QY 77 GlnCysSerProAspLeuArgPheAspLeuLysCysThrMetYrrThrProIleCysLeuPro 96
 Db 121 CGCTGCCTCCCGGACCTGCTCTCTGAGCACCCCCATCTGCCCTGCGCC 180
 QY 97 AspPTyrHisLysProLeuProProCysArgSerValCysGluArgAlaLysAlaGlyCys 116
 Db 181 GACTACGGCAGGCCCTGCCCTCCGCTGCTGAGCGGCCAGCAGGGCTGC 240
 QY 117 SerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAspArgLeu 136
 Db 241 TCCCCGCTGTGAGCCAGTGGCCCTGAGTGGCCGAGGAGTAGCTGCGAGAGCTG 300
 QY 137 ProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAspArgSerGluAlaThr 156
 Db 301 CCCCACTGGCC----GACGAGGCTCTGAGCATGGACCAAGCAGGAGTCACC 354
 QY 157 Thr---Ala-ProProArgProProProAlaLysProThrLeuProGlyProGly 175
 Db 355 ACCCTGGGTCCACCTTCCCCAACCCACCCCAAGGTCAGAGCAGGAGGCCGCC 414
 QY 175 aProAlaSerGlyGlyGluCysProAlaGlyGlyProPheValCysAlaCysBrgiuPr 195
 Db 415 GCCCAGTGTGAGGGAG-----TCCGCCTTCGACTT 449
 QY 195 oPheValProLeuLysGluSerHisProLeuYrasLysValArgThr----- 212
 Db 450 CCTGGTCCCATTCCGGAGGGRGCBCCTCCGCCCTACAGCACGCCGGSBCGGCCCCGG 509
 QY 213 -----GlyGlnValProAsnCysAlaValProCysTyrGlnPr 225
 Db 510 CCCCGCCCCGGCCGGCCGGCCGCCGCCCCAGCTGGCCCTGCCACAGGCC 569
 QY 225 oSerPheserAlaAspPheGluArgThr-Phe 234
 Db 570 CTCTCTCACGGAGGAGCAGCTTC 597

RESULT 4
 BB625724/C
 LOCUS BB625724
 DEFINITION RIKEN full-length enriched, adult male diencephalon Mus musculus cDNA clone 933012118 5', mRNA sequence.
 VERSION BB625724

FEATURES
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 /organism="Tetraodon nigroviridis"
 /db_xref="taxon:98883"
 /clone="183G18"
 /clone_lib="G"
 /note="Genoscope sequence ID : COAG183BD091P1-end : T7"
 BASE COUNT 143 a 393 c 301 g 185 t 6 other_B
 ORIGIN ORIGIN
 Alignment Scores:
 Pred. No.: 2.98e-44 Length: 1028
 Score: 653.50 Matches: 129
 Percent Similarity: 68.57% Conservative: 15
 Best Local Similarity: 61.43%
 Query Match: 49.89% MisMatches: 44
 DB: 17 Gaps: 23
 US-09-847-102A-68 (1-235) x CNS02ZUH (1-1028)

QY 37 ThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsn 56
 Db 1 ACGGTCCCCATGGCAGGACATCGCTACACCTACATGCCAACCGAGTCAC 60
 QY 57 HisAspPThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGluIle 76
 Db 61 CACGAGACCCAGGAGGAGGAGGCTGAGGTGACCCAGTCTGGCCCTGTGCGTATC 120
 QY 77 GlnCysSerProAspLeuArgPheAspLeuLysCysThrMetYrrThrProIleCysLeuPro 96
 Db 121 CGCTGCCTCCCGGACCTGCTCTCTGAGCACCCCCATCTGCCCTGCGCC 180
 QY 97 AspPTyrHisLysProLeuProProCysArgSerValCysGluArgAlaLysAlaGlyCys 116
 Db 181 GACTACGGCAGGCCCTGCCCTCCGCTGCTGAGCGGCCAGCAGGGCTGC 240
 QY 117 SerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAspArgLeu 136
 Db 241 TCCCCGCTGTGAGCCAGTGGCCCTGAGTGGCCGAGGAGTAGCTGCGAGAGCTG 300
 QY 137 ProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAspArgSerGluAlaThr 156
 Db 301 CCCCACTGGCC----GACGAGGCTCTGAGCATGGACCAAGCAGGAGTCACC 354
 QY 157 Thr---Ala-ProProArgProProProAlaLysProThrLeuProGlyProGly 175
 Db 355 ACCCTGGGTCCACCTTCCCCAACCCACCCCAAGGTCAGAGCAGGAGGCCGCC 414
 QY 175 aProAlaSerGlyGlyGluCysProAlaGlyGlyProPheValCysAlaCysBrgiuPr 195
 Db 415 GCCCAGTGTGAGGGAG-----TCCGCCTTCGACTT 449
 QY 195 oPheValProLeuLysGluSerHisProLeuYrasLysValArgThr----- 212
 Db 450 CCTGGTCCCATTCCGGAGGGRGCBCCTCCGCCCTACAGCACGCCGGSBCGGCCCCGG 509
 QY 213 -----GlyGlnValProAsnCysAlaValProCysTyrGlnPr 225
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 QY 225 oSerPheserAlaAspPheGluArgThr-Phe 234
 Db 570 CTCTCTCACGGAGGAGCAGCTTC 597

KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Takanami,M., Tagawa,A., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL	RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
COMMENT	Unpublished (2001) Contract: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp URL: http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. <i>Genome Res.</i> 10 (10), 1617-1630 (2000)
BASE COUNT	130 a
ORIGIN	BambiI
ALIGNMENT SCORES:	
PRED. NO.:	2.21e-44
SCORE:	652.00
LENGTH:	653
CONSERVATIVE:	1
PERCENT SIMILARITY:	99.17%
BEST LOCAL SIMILARITY:	98.33%
QUERY MATCH:	49.77%
DB:	10
GAPS:	0
US-09-847-102A-68 (1-235) x BB625724 (1-653)	
QY	1 MetAlaArgProAspProSerAlaProProSerLeuLeuLeuLeuLeuLeuAlaLeu 20
DB	363 ATGGCUCGACGCCGACCCGCTCGGCCTCTCTCTCTCTGCTGCTGCTGCGCGAGCTG 304
QY	21 ValGlyArgAlaAlaAlaAlaAlaSerLysAlaProValCysGlnGluLeuThrValProMet 40
DB	303 GTGGGCCGGGAGCCGCCGCTCGGCCTCTCTCTGCTGCTGCTGCTGCGCGAGCTG 244
QY	41 CYSA[TG]GlyIleGlyIleGlyIleAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
DB	243 TGCCGAGCATGGCTACAACCTGAGCACATGCCAACAGTTCACATGAACAGCAG 184
QY	61 AspGluLysAlaGlyLeuLysValHisGlnPheIleProLeuValGluarginCysSerPro 80
DB	183 GACGAAGCAGAGCCTGGAGGAGCACCAATCTGGCGCTTGAGATTCCACTGCTCACCG 124
QY	81 AspLeuArgphePheIleCysThrMetTYThrProIleCysLeuProAspTYHisLYS 100
DB	123 GACCTGGCTCTCTGTGCTATGTACGCCATCTGTTGCTTGACTACCACAG 64
QY	101 ProLeuProProCysArgSerValCysGluArgAlaLysAlaGlyCysSerProLeuMet 120
DB	63 CGCTTACACGGTGCGTGGTGGAGGGGCCAAAGCCGGGTGCTGCCGGTCATG 4
RESULT	5
BB622817	
DEFINITION	BB622817 RIKEN full-length enriched, adult male olfactory brain Mus musculus cDNA clone 6430550619 5 , mRNA sequence.
ACCESSION	BB622817
VERSION	BB622817.1 GI:15397890
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Takanami,M., Tagawa,A., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE	Unpublished (2001)
JOURNAL	RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp

LOCUS	BG438433	564 bp mRNA linear EST 10-MAY-2001	Db	265 AACCAATTCAACCCACAAACCCAGAAGGAGCCGCATGGAACTGCCAGTGTGGCG 324
DEFINITION	pe25d03_y2 Trichinella spiralis ML CMVsport jaesmer Trichinella spiralis cDNA 5' similar to TR:Q13467 Q13467 TRANSMEMBRANE RECEPTOR ; mRNA sequence.	Qy	73 LeuvalGluileglnGlyssrprorprleuargphepheeuCysThrhetTyrrThrPro 92	
ACCESSION	BG438433		Db	325 CTGGTGAAATCAACTGCACTCCGGATTTCGTTTCTGAGCATGACGCC 384
VERSION	BG438433.1	GT:13348081		
KEYWORDS	EST; Trichinella spiralis; Trichinellidae; Trichinella.			
REFERENCE	1 (bases 1 to 564)			
AUTHORS	Mc Carter,J., Clifton,S., Chiapelli,B., Rape,D., Martin,J., Wylie,T., Dant,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Septoe M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.			
TITLE	The Washington Univ. Nematode EST Project, 1999			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: McCarter JP			
FEATURES	source			
source	1. .564 Location/Qualifiers			
/organism="Trichinella spiralis"				
/db_xref="taxon:6334"				
/clone_libr="Trichinella spiralis ML CMVsport jaesmer"				
/dev_stage="muscle stage larvae"				
/lab_host="DH10B"				
/note="Vector: pCMVSPORT-7.neo; Site_1: NotI; Site_2: SalI ; The library was constructed using mRNA isolated from total RNA with oligo-dT cellulose. Total RNA was generated from muscle larvae that were isolated from infected rats. Larvae were liberated by pepsin/HCl digestion, incubated with 1% SDS, treated with RNase and DNase to eliminate host nucleic acid contamination, and purified on a Percoll gradient. The T. spiralis isolate was obtained from Dickson Despommier (Columbia University). The library was provided by Dr. Doug Jasmer (djasmer@vetmed.wsu.edu) and colleagues at Washington State University. DNA sequencing by: Washington University Genome Sequencing Center St. Louis."				
BASE COUNT	144 a 151 c 149 g 120 t			
ORIGIN				
Alignment Scores:				
Pred. No.:	1e-34	Length: 564		
Score:	534.50	Matches: 69		
Percent Similarity:	86.79%	Conservative: 16		
Best Local Similarity:	73.55%	Mismatches: 15		
Query Match:	40.80%	Indels: 1		
DB:	12 Gaps: 1			
US-09-847-102A-68 (1-235) x BG438433 (1-564)				
FEATURES	source			
source	1. .559 Location/Qualifiers			
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/clone_libr="Trichinella spiralis ML CMVsport jaesmer"				
/dev_stage="muscle stage larvae"				
/lab_host="DH10B"				
/note="Vector: pCMVSPORT-7.neo; Site_1: NotI; Site_2: SalI ; The library was constructed using mRNA isolated from total RNA with oligo-dT cellulose. Total RNA was generated from muscle larvae that were isolated from infected rats. Larvae were liberated by pepsin/HCl digestion, incubated with 1% SDS, treated with RNase and DNase to eliminate host nucleic acid contamination, and purified on a Percoll gradient. The T. spiralis isolate was obtained from				
OY	33 CysGingluleiIethralValPrometCysArgGlyIieglyTyrAspLeuThrRhsmetPro 52			
Percent Similarity:	86.79%			
Best Local Similarity:	73.55%			
Query Match:	40.80%			
DB:	205 GTCAGGAGAGTCATCCCCATGCAAGTCATGACCAAATGCC 264			
OY	53 ArgGlnPheasnHiGasptingnaspGlnLalGlyLeudluvalHisGlnPheHtpPro 72			

Dickson Despommier (Columbia University). The library was provided by Dr. Doug Jasmer (djasmer@vetmed.wsu.edu) and colleagues at Washington State University DNA Sequencing by: Washington University Genome Sequencing Center St. Louis."

BASE COUNT
ORIGIN
143 a 147 c 148 g 120 t 1 others

Alignment Scores:
Pred. No.: 6.66e-34
Score: 524.50
Percent Similarity: 85.71%
Best Local Similarity: 74.79%
Query Match: 40.04%
DB: 12

US-09-847-102a-68 (1-235) x BG353236 (1-559)

Qy 33 CysGlnGluLeuThrValProMetCysArgGlyIleGlyTrpAspLeuThrHisMetPro 52
Db 206 TGTGAGGAGATGCACTCCGATGTCGATCGCTACATTAGACCCTAATGCC 265

Qy 53 AsnGlnPheAsnHiSASPThrGlnAspGluAlaGlyLeuGluValHiSASPheTerPro 72
Db 266 AACCAATTCAACCAACCCAAAGAGAAACGGCATGGAGTGCACCAAGCTCGCCG 325

Qy 73 LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetTyrThrPro 92
Db 326 CTGGTCGAATCAACTGCACTGGAGTTGGTTTCTCTGACCATGTCACGCCG 385

Qy 93 IleCysLeuProAspThrHisLysProLeuProProCysAspGlySerValCysGluArgAla 112
Db 386 ATTGCAATAGCGATTATCCGAACCGTTGCCGCTGCAAGCTGGATGCGAACGCC 445

Qy 113 LysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluIargMetSer 132
Db 446 AAGGCCGCTGGGCCACTGATGCCAGTAGCGTTTCGATGGGCCCAATTGGAC 505

RESULT 10

LOCUS AI892150 603 bp mRNA linear EST 15-MAR-2000
DEFINITION mh41e05_Y1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA
clone IMAGE:45088 5' similar to TR:Q13467 TRANSMEMBRANE
RECEPTOR. ; mRNA sequence.

ACCESSION AI892150
VERSION AI892150.1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mamilla (bases 1 to 603)

REFERENCE 1 Marras, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steppone, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT Contact: Marras M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mousebest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone. This read has been verified (found to hit its original self in the

correct orientation)
possible reversed clone: similarity on wrong strand
MG3:270424
Seq primer: -40R from Gibco
High quality sequence stop: 437.
Location/Qualifiers
/note="organism:placenta; vector: pRT3D-Pac (Pharmacia)
with a modified polylinker; Site1: Not I; Site2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dt) primer
[5' TGTACCAACTCTGAGTGGAGGGCCGGAAATTTTTTTTTTTTTTTTTT
T 3']"; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library
went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
/dev_stag="adult".
/lab_host="DH110B"

BASE COUNT
ORIGIN
125 a 157 c 217 g 101 t 3 others

RESULT 11

LOCUS BB718107 571 bp mRNA linear EST 12-SEP-2000
DEFINITION RCL-HT0797-210600-021-d10 Rn0797 Homo sapiens cDNA, mRNA sequence.
ACCESSION BB718107
VERSION BB718107.1 GI:10106372
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Qy 119 LeuMetArgInTyrglyPheAlaTrpProGluIargMetSerCysAspArg-LeuPro 138
Db 603 CTCTATGCCAGTACCGCTTGCCCTGGCCAGCGCATGAGCTGGACCCACCTCTG 544

Qy 138 allelenglyArgAsp-AlaGluLeuCysMetAspTygAspArgSerGluAlaThrThr 157
Db 543 TCTGGCGACGCCNNAGGTTCTGTGATGGAAATAACCGAAGCGAACACCAAC 484

Qy 158 AlaProProArgProPheProAlaLysProThrIleProGlyProProGlyAlaProAla 177
Db 483 GGGTCCTGTAAGTCCTCCCCGGGCCACTTACACTCACAGAACGCCAGGGNCATCT 424

Qy 178 SerGlyGlyGluCysProAlaIglyGlyProPheValCysLySArgGluProPheVal 197
Db 423 TCCGGGGCGGAGGTCGCCCTCGGAGGCCATCCGTCGACGTGCGGCCAGGCTCTG 364

Qy 198 ProIleLeuIgylsGlySerHisProLeuIysValArgThrGlyGlyInvalProAsn 217
Db 363 CCCATCTGAAAGGAGTCACCCACTCTTACACAAGGTGCGCACCGGCCAGTGCAC 304

Qy 218 CysAlaValProCysTyrGlnProSerPheSerAlaAspGluAqGlyPheAla 235
Db 303 TAGGGGGTGCCCTGCTTACACAGCCGGGACGCCACTTCGCC 250

REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1' (bases 1 to 571)		
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nacai, M.A., da Silva, W. Jr., Zago, M.A., Bordim, S., Costa, F.F., Goldmann, G.H., Carvalho, A.P., Matukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bicher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
MEDLINE	200202663		
COMMENT	Contact: Simpson, A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br		
SOURCE	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/g/gethtml2.pl?l1=&t2=RC1-HT0737-210600-021&t3=2000-06-21&t41)		
FEATURES	<p>Seq primer: puc 18 forward High quality sequence start: 29 High quality sequence stop: 543.</p> <p>Location/Qualifiers</p> <ol style="list-style-type: none"> 1. 571 		
BASE COUNT	118 a 165 c 192 g 96 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	4.56e-32	Length:	571
Score:	502.50	Matches:	86
Percent Similarity:	88.14%	Conservative:	18
Best Local Similarity:	72.88%	Mismatches:	12
Query Match:	38.36%	Indels:	2
DB:	12	Gaps:	1
US-09-847-102A-68 (1-235) x BE718107 (1-571)			
Qy	33 CysGlnGluIleThrValProMetCysBarglyfleGlyTyrAsnLeuThrHisMetPro	Db	52
Db	95 TCGGAGGAGATCACCATCCATGTCGGCATGGCTACATCCTCTCCC	DEFINITION	RESULT 12
Qy	53 AsnGlnPheAsnHisAspThrGlnAspGlnAlaGlyLeuGluValHisGlnPheThrPro	ACCESSION	A1958244
Db	155 AACGAGATGAACATAGAACGAGACCAAGCAGGAGAAAGGGGCCTGGGGTGTGGCC	KEYWORDS	AI958244 mRNA
Qy	73 LeuValGluIleGlyCysSerProAspLeuPhePheLeuCysThrMetTyrThrPro	ORGANISM	AI958244 Zebratfish
Db	215 CTGGTGGAGATCAATGCTCCGGACCTCAAGTCTCTCCGTGCAAGTACAGGCC	SOURCE	Danio rerio
Qy	93 IleCysLeuProAspTyrIleLysProLeuProProCysArgSerValCysGluArgGala	REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
Db	275 ATCTGCTGGAGATCCGACCCATATGAGCAGCTGCTGAGAGAGCC	AUTHORS	Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy ; K., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyllie, T., Underwood ; K., Sheptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Smaller, T., Gibbons, M., Pace, D., Harvey, N., Schurk, R., Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Qy	113 IysValAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProIuargMetSer	TITLE	WashU Zebrafish EST Project 1998
Db	335 CGCTCGGATGCCACCATATGAGCAGCTGCTGAGAGAGATGGCG	JOURNAL	Unpublished (1998)
FEATURES			
SOURCE			
COMMENT	Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: zebrafish@wustl.wustl.edu		
FEATURES			
SOURCE	CDNA Library Preparation: Matthew Clark. CDNA library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center. Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.regen.com) (email contact: info@regen.com) and Ressourcenzentrum PrimärDatenbank, Berlin, Germany (web address: www.rzpd.de)		
FEATURES	Possible reversed clone: similarity on wrong strand		
SOURCE	Seq primer: T3 ER from Amersham High quality sequence stop: 496.		
FEATURES			
SOURCE			
COMMENT	Seq primer: T3 ER from Amersham High quality sequence stop: 496.		
FEATURES			
SOURCE			
COMMENT			
Qy	1. 679	Db	133 CysAspArgLeu-ProValLeuGlyArgAspAlaGluValLeuCysMetAsp
Db	/db xref="IMAGe:3799704"	DEFINITION	679 bp mRNA linear EST 07-JUN-2001
DEFINITION	/clone lib="IMAGe:3799704"	IMAGE	fd02c05.y1 Zebratfish WashU MPIG EST Danio rerio cDNA clone 443
IMAGE	/clone lib="IMAGe:3799704"	mRNA sequence.	3/229704 5, similar to TR:061091 061091 FRIZZLED HOMOLOG 8 ,
COMMENT			

BASE COUNT 147 a 191 c 182 g 156 t 3 others
 ORIGIN
Alignment Scores:
 Pred. No.: 7.4e-30 Length: 679
 Score: 47.00 Matches: 85
 Percent Similarity: 83.04% Conservative: 8
 Best Local Similarity: 75.89% Mismatches: 19
 Query Match: 36.41% Indels: 0
 DB: 9 Gaps: 0

US-09-847-102a-68 (1-235) x A1958244 (1-679)

QY 13 LeuLeuLeuLeuLeuLeuAlaGlnLeuValGlyArgGalaAlaAlaLaserLeuAlaProVal 32
 Db 338 CTCCTCCGCGCTGCGTCACTGCCCGATGAGCGGTACACGGCCAAGGAGTCAC 397

QY 33 CysGlnGluIleThrValProMetCYSArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
 Db 398 TGTCAAGGAGATGCCGGTCCGGTGGAAGGSGATCGTTAACTACACTACATGCC 457

QY 53 AsnGlnPheAspHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpPro 72
 Db 458 AACGAGTCACACAGCACGAGGAGAAGCGGTTGGAGCTGACCAAGCTCGCT 517

QY 73 LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysthrMetTyrThrPro 92
 Db 518 CTCGTGGAGATCAGTCAGTCCTCCGGATCTCAAGTCCTCTCTGCAACATGACCCG 577

QY 93 IleCysLeuProAspTyrHisLysProLeuProProCYSArgSerValCysGluArgAla 112
 Db 578 ATATGCCTGGAGGACTTAAGANACCCCTTNGCCGCGAGCAGCTGAGAGAGCC 637

QY 113 LysAlaGlyCysSerProLeuMetArgGlnTyrGly 124
 Db 638 AACGGCGGCTGGCCCGCTCTGCGCANTACGGG 673

RESULT 13
 BB619404 LOCUS BB619404 DEFINITION 607 bp mRNA linear EST 31-AUG-2001
 ACCESSION BB619404
 VERSION BB619404.1
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 607)
 AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanasaki,T., Hara,A.,
 , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,
 M., Koya,S., Matsuyama,T., Miyakai,A., Nomura,K., Ohno,M.,
 Okazaki,T., Orido,T., Saito,R., Sakai,K., Sanjo,H., Sasaki,
 D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
 Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
 Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Yoshinobu Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-resgsc.rikken.go.jp/
 URL: http://genome.gsc.rikken.go.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,
 M., Kondo,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. . 10 (10), 1617-1630 (2000)

BASE COUNT 95 a 222 c 179 g 111 t
 ORIGIN
Alignment Scores:
 Pred. No.: 1.36e-28 Length: 607
 Score: 461.00 Matches: 92
 Percent Similarity: 59.69% Conservative: 25
 Best Local Similarity: 46.94% Mismatches: 57
 Query Match: 35.19% Indels: 22
 DB: 10 Gaps: 7

US-09-847-102a-68 (1-235) x BB619404 (1-607)

QY 33 CysGlnGluIleThrValProMetCYSArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
 Db 51 TGCCAGCCCATCTCCATCCGCTGCGACAGCATGCCAACAGACATGCC 110

QY 53 AsnGlnPheAspHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpPro 72
 Db 111 AACCTCTTGGCCACAGGAACCAGGAAGACGGCGGGCCCTGGAGGSGATCATGTTCTACCCG 170

QY 73 LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysthrMetTyrThrPro 92
 Db 171 CTGGTGAAGGTCGCTGCTGCCGAGCTGCCTCTCTCTGTCATGACCGCCG 230
 QY 93 IleCysLeuProAspTyrHisLysProLeuProProCYSArgSerValCysGluArgAla 112

wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
 Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Masuura,
 S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
 Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Konno,H., Fukunishi,J., Shibata,K., Itoh,M., Carninci,P., Sugahara,
 Y. and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Yamanka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa,
 K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T.,
 Ishii,Y. and Hayashizaki,Y.
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
 Func. Genomics 2 pre, 172-186 (2001)
 Please visit our web site (<http://genome.gsc.rikken.go.jp>) for
 further details.
 e mouse tissues.
FEATURES
 source /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon::0090"
 /clone_id="573042E22"
 /clone lib="RIKEN full-length enriched, 8 days embryo"
 /sex="mixed"
 /dev_stage="8 days embryo"
 /lab_host="DNI0B"
 /note="Site 1: SAI1; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGATCCAGAGCTTTTTTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of subtraction to
 Rot = 100. Second strand cDNA was prepared with the
 primer adapter of sequence [5'
 GAGAGAGAGATCCAGAGCTTTAATCCCCCCCC 3']. cDNA
 was cloned into the XhoI and BamHI sites. Vector: a
 modified pBluescript KS(+) after bulk excision from Lambda
 FLC 1. Cloning sites, 5' end: SAI1; 3' end: BamHI."

Melkonyan, Rosep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US10/146,474
FILING DATE: 14-MAY-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US10/937,067
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Lehnbrat, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLogy: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-146-474-9
Query Match
Best Local Similarity 100.0%; Score 1310; DB 25; length 585;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARPDPSAPPSSLLILLQLVGRARAASKAPVCQETIVPMCRGIGNLTHMPNQFNHDQ 60
Db 1 MARPDPSAPPSSLLILLQLVGRARAASKAPVCQETIVPMCRGIGNLTHMPNQFNHDQ 60
Qy 61 DEAGLEYHQFWPLVEIQCSPDRFLFLCTMYTPICLDPYHKPLPPCRSVCERAKAGCSPLM 120
Db 61 DEAGLEYHQFWPLVEIQCSPDRFLFLCTMYTPICLDPYHKPLPPCRSVCERAKAGCSPLM 120
Qy 121 RQGFAMPERMSCDRLPVLGRDAEVLCMDYRNSEATTAAPRPFPAKPTLPGPGAPASGG 180
Db 121 RQGFAMPERMSCDRLPVLGRDAEVLCMDYRNSEATTAAPRPFPAKPTLPGPGAPASGG 180
Qy 181 ECPAGGPVCKCREPFVILKESHLPLNKVRGQVNCAVPCYQPSFSADERTFA 235
Db 181 ECPAGGPVCKCREPFVILKESHLPLNKVRGQVNCAVPCYQPSFSADERTFA 235

US-10-146-474-9

RESULT 6
US-08-832-340-10
Sequence 10, Application US/08832340
GENERAL INFORMATION:

APPLICANT: Bhanot, Purrima
APPLICANT: Brink, Marcel
APPLICANT: Harryman, Cindy S.
APPLICANT: Wang, Yanshu
APPLICANT: Hsieh, Jen-chih
APPLICANT: Andrew, Deborah
APPLICANT: Nathans, Jeremy

APPLICANT: Nusse, Roel
TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Delbinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US10/832,340
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/015,307
FILING DATE: 12-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 39,615
REFERENCE/DOCKET NUMBER: 8600-0167.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 586 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLogy: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Hf25 protein

US-08-832-340-10

Query Match
Best Local Similarity 100.0%; Score 1310; DB 12; length 586;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARPDPSAPPSSLLILLQLVGRARAASKAPVCQETIVPMCRGIGNLTHMPNQFNHDQ 60
Db 1 MARPDPSAPPSSLLILLQLVGRARAASKAPVCQETIVPMCRGIGNLTHMPNQFNHDQ 60
Qy 61 DEAGLEYHQFWPLVEIQCSPDRFLFLCTMYTPICLDPYHKPLPPCRSVCERAKAGCSPLM 120
Db 61 DEAGLEYHQFWPLVEIQCSPDRFLFLCTMYTPICLDPYHKPLPPCRSVCERAKAGCSPLM 120
Qy 121 RQGFAMPERMSCDRLPVLGRDAEVLCMDYRNSEATTAAPRPFPAKPTLPGPGAPASGG 180
Db 121 RQGFAMPERMSCDRLPVLGRDAEVLCMDYRNSEATTAAPRPFPAKPTLPGPGAPASGG 180
Qy 181 ECPAGGPVCKCREPFVILKESHLPLNKVRGQVNCAVPCYQPSFSADERTFA 235
Db 181 ECPAGGPVCKCREPFVILKESHLPLNKVRGQVNCAVPCYQPSFSADERTFA 235

RESULT 7
US-08-832-340-10

Sequence 10, Application US/10152348
GENERAL INFORMATION:

APPLICANT: Bhanot, Purrima
APPLICANT: Brink, Marcel
APPLICANT: Harryman, Cindy S.
APPLICANT: Wang, Yanshu
APPLICANT: Hsieh, Jen-chih
APPLICANT: Andrew, Deborah
APPLICANT: Nathans, Jeremy

Nathans, Jeremy
Nusse, Roel

TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPILER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/152,548
FILING DATE: 21-MAY-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-APR-1997
APPLICATION NUMBER: US 60/015,307
FILING DATE: 12-APR-1996

ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0167.30

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 586 amino acids

TYPE: amino acid
STRANDEDNESS: single
INDIVIDUAL ISOLATE: Hfz5 protein

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-152-548-10

Query Match 100.0% Score 1310; DB 25; Length 586;
Best Local Similarity 100.0%; Pred. No. 2e-101; Mismatches 235; Conservative 0; Indels 0; Gaps 0; Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPDPSAPSLLILLALQVGRARAASKAASKAPVCOEITVPMCGRGIGNLTHMPNQFNHTQ 60
Db 1 MARPDPSAPSLLILLALQVGRARAASKAASKAPVCOEITVPMCGRGIGNLTHMPNQFNHTQ 60

QY 61 DEAGLEHQFWPLVEIQCSPPDRFLCTMYTPICLPDPYHKPLPPCRSVCERAKAGCSPLM 120
Db 61 DEAGLEHQFWPLVEIQCSPPDRFLCTMYTPICLPDPYHKPLPPCRSVCERAKAGCSPLM 120

QY 121 ROYGFAPWPERMSCDRLPVGLRDAVLCMDYNRSATTAAPRPFPAKPTLPGPGAPASGG 180
Db 121 ROYGFAPWPERMSCDRLPVGLRDAVLCMDYNRSATTAAPRPFPAKPTLPGPGAPASGG 180

QY 181 ECPAGGPVCKCREFPVILKESHLPLYNKVRTGQVNCAPVCPYQPSFSADERTPA 235
Db 181 ECPAGGPVCKCREFPVILKESHLPLYNKVRTGQVNCAPVCPYQPSFSADERTPA 235

QY 181 ECPAGGPVCKCREFPVILKESHLPLYNKVRTGQVNCAPVCPYQPSFSADERTPA 235
Db 181 ECPAGGPVCKCREFPVILKESHLPLYNKVRTGQVNCAPVCPYQPSFSADERTPA 235

RESULT 9
US-60-207-360-270

Sequence 270, Application US/60207360

GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED RECEPTORS, NUCLEAR ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000591

APPLICANT: Harriman, Cindy S.
APPLICANT: Wang, Yanshu
APPLICANT: Hsieh, Jen-chin
APPLICANT: Andrew, Deborah
APPLICANT: Nathans, Jeremy
APPLICANT: Nusse, Roel

TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPILER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-APR-1997
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 586 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Hfz5 protein

US-60-015-307-10

Query Match 100.0% Score 1310; DB 27; Length 586;
Best Local Similarity 100.0%; Pred. No. 2e-101; Mismatches 235; Conservative 0; Indels 0; Gaps 0; Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPDPSAPSLLILLALQVGRARAASKAASKAPVCOEITVPMCGRGIGNLTHMPNQFNHTQ 60
Db 1 MARPDPSAPSLLILLALQVGRARAASKAASKAPVCOEITVPMCGRGIGNLTHMPNQFNHTQ 60

QY 61 DEAGLEHQFWPLVEIQCSPPDRFLCTMYTPICLPDPYHKPLPPCRSVCERAKAGCSPLM 120
Db 61 DEAGLEHQFWPLVEIQCSPPDRFLCTMYTPICLPDPYHKPLPPCRSVCERAKAGCSPLM 120

QY 121 ROYGFAPWPERMSCDRLPVGLRDAVLCMDYNRSATTAAPRPFPAKPTLPGPGAPASGG 180
Db 121 ROYGFAPWPERMSCDRLPVGLRDAVLCMDYNRSATTAAPRPFPAKPTLPGPGAPASGG 180

QY 181 ECPAGGPVCKCREFPVILKESHLPLYNKVRTGQVNCAPVCPYQPSFSADERTPA 235
Db 181 ECPAGGPVCKCREFPVILKESHLPLYNKVRTGQVNCAPVCPYQPSFSADERTPA 235

RESULT 9
US-60-207-360-270

Sequence 270, Application US/60207360

GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED RECEPTORS, NUCLEAR ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000591

CURRENT APPLICATION NUMBER: US/60/207,360
 CURRENT FILING DATE: 2000-05-26
 NUMBER OF SEQ ID NOS: 386
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 270
 LENGTH: 526
 TYPE: PRT
 ORGANISM: HUMAN
 US-60-207-360-270

Query Match Best Local Similarity 99.7%; Score 1306; DB 27; Length 526; Matches 234; Conservative 99.6%; Pred. No. 3..9e-101; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPPDSAPPSSLLILQLVGRAGAAASKAPVQCBETVPMCRGIGYNLTHMPNQFNHDQ 60
 Db 1 MARPPDSAPPSSLLILQLVGRAGAAASKAPVQCBETVPMCRGIGYNLTHMPNQFNHDQ 60

QY 61 DEAGLEHQFWPLVLEIQCSPDRLVGRDAEVLMYRFLCTMYTPICLPDYHKPKLPPCRSVCERAKAGCPLM 120
 Db 61 DEAGLEHQFWPLVLEIQCSPDRLVGRDAEVLMYRFLCTMYTPICLPDYHKPKLPPCRSVCERAKAGCPLM 120

QY 121 ROYGFAAERMSCDRRLPVLGRDAEVLMYRFLCTMYTPICLPDYHKPKLPPCRSVCERAKAGCPLM 180
 Db 121 ROYGFAAERMSCDRRLPVLGRDAEVLMYRFLCTMYTPICLPDYHKPKLPPCRSVCERAKAGCPLM 180

QY 181 ECPAGGPVCKREPFVPILKESHPLYNKVRQAVPCVQPSFSADERTFA 235
 Db 181 ECPAGGPVCKREPFVPILKESHPLYNKVRQAVPCVQPSFSADERTFA 235

RESULT 10
 US-60-229-515-752 Sequence 752, Application US/60229515
 ; GENERAL INFORMATION:
 ; APPLICANT: Beasley, Ellen
 ; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
 ; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
 ; FILE REFERENCE: CL000776
 ; CURRENT APPLICATION NUMBER: US/60/229,515
 ; CURRENT FILING DATE: 2000-09-05
 ; NUMBER OF SEQ ID NOS: 2013
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 752
 ; LENGTH: 542
 ; TYPE: PRT
 ; ORGANISM: HUMAN
 US-60-229-515-752

Query Match Best Local Similarity 99.7%; Score 1306; DB 27; Length 542; Matches 234; Conservative 99.6%; Pred. No. 4e-101; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPPDSAPPSSLLILQLVGRAGAAASKAPVQCBETVPMCRGIGYNLTHMPNQFNHDQ 60
 Db 1 MARPPDSAPPSSLLILQLVGRAGAAASKAPVQCBETVPMCRGIGYNLTHMPNQFNHDQ 60

QY 61 DEAGLEHQFWPLVLEIQCSPDRLVGRDAEVLMYRFLCTMYTPICLPDYHKPKLPPCRSVCERAKAGCPLM 120
 Db 61 DEAGLEHQFWPLVLEIQCSPDRLVGRDAEVLMYRFLCTMYTPICLPDYHKPKLPPCRSVCERAKAGCPLM 120

QY 121 ROYGFAAERMSCDRRLPVLGRDAEVLMYRFLCTMYTPICLPDYHKPKLPPCRSVCERAKAGCPLM 180
 Db 121 ROYGFAAERMSCDRRLPVLGRDAEVLMYRFLCTMYTPICLPDYHKPKLPPCRSVCERAKAGCPLM 180

QY 181 ECPAGGPVCKREPFVPILKESHPLYNKVRQAVPCVQPSFSADERTFA 235
 Db 181 ECPAGGPVCKREPFVPILKESHPLYNKVRQAVPCVQPSFSADERTFA 235

RESULT 11
 US-09-847-102A-38 Sequence 38, Application US/09847102A
 ; GENERAL INFORMATION:
 ; APPLICANT: University of California
 ; APPLICANT: Carson, Dennis A.
 ; APPLICANT: Corr, Maripat
 ; APPLICANT: Rhee, Chae-Seo
 ; APPLICANT: Lorenzo, Leoni M.
 ; APPLICANT: Malini, Sen
 ; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
 ; CURRENT FILING DATE: 2001-05-01
 ; CURRENT APPLICATION NUMBER: US/09/847,102A
 ; CURRENT FILING DATE: 2000-20629-00
 ; FILE REFERENCE: 2000-20629-00
 ; NUMBER OF SEQ ID NOS: 138
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 38
 ; LENGTH: 516
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-847-102A-38

Query Match Best Local Similarity 94.8%; Score 111; DB 22; Length 516; Matches 205; Conservative 87.2%; Pred. No. 1e-84; Mismatches 0; Indels 30; Gaps 1;

QY 1 MARPPDSAPPSSLLILQLVGRAGAAASKAPVQCBETVPMCRGIGYNLTHMPNQFNHDQ 60
 Db 1 MARPPDSAPPSSLLILQLVGRAGAAASKAPVQCBETVPMCRGIGYNLTHMPNQFNHDQ 60

QY 61 DEAGLEHQFWPLVLEIQCSPDRLVGRDAEVLMYRFLCTMYTPICLPDYHKPKLPPCRSVCERAKAGCPLM 120
 Db 61 DEAGLEHQFWPLVLEIQCSPDRLVGRDAEVLMYRFLCTMYTPICLPDYHKPKLPPCRSVCERAKAGCPLM 120

QY 121 ROYGFAAERMSCDRRLPVLGRDAEVLMYRFLCTMYTPICLPDYHKPKLPPCRSVCERAKAGCPLM 180
 Db 121 ROYGFAAERMSCDRRLPVLGRDAEVLMYRFLCTMYTPICLPDYHKPKLPPCRSVCERAKAGCPLM 180

QY 181 ECPAGGPVCKREPFVPILKESHPLYNKVRQAVPCVQPSFSADERTFA 235
 Db 181 ECPAGGPVCKREPFVPILKESHPLYNKVRQAVPCVQPSFSADERTFA 235

RESULT 12
 US-60-213-169-237 Sequence 237, Application US/60213169
 ; GENERAL INFORMATION:
 ; APPLICANT: BEASLEY, ELLEN
 ; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
 ; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
 ; FILE REFERENCE: CL000659
 ; CURRENT APPLICATION NUMBER: US/60/213,169
 ; CURRENT FILING DATE: 2000-06-22
 ; NUMBER OF SEQ ID NOS: 678
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 237
 ; LENGTH: 232
 ; TYPE: PRT
 ; ORGANISM: HUMAN
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)..(232)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 US-60-213-169-237

Query Match Best Local Similarity 99.4%; Score 1014; DB 27; Length 232; Matches 178; Conservative 98.3%; Pred. No. 6.2e-77; Mismatches 1; Indels 0; Gaps 0;

QY 55 FHNDTDEAGLEHQFWPLVLEIQCSPDRLVGRDAEVLMYRFLCTMYTPICLPDYHKPKLPPCRSVCERAKA 114
 Db 1 FHNDTDEAGLEHQFWPLVLEIQCSPDRLVGRDAEVLMYRFLCTMYTPICLPDYHKPKLPPCRSVCERAKA 60

Qy 115 GCSPLMROQGFAWPERMSCDRLPVGDAEVLCMDYNRSSEATTAPRPRPAKPTLPGPGC 174
Db 61 GCSPLVLRQFGFAPWERMSCDRLPVGDAEVLCMDYNRSSEATTAPRPRPAKPTLPGPGC 120
Qy 175 APASGGECPAGGPVCKCERBPFLVILKESHLINKYRTGQVNCAPCYQPSFSADERTF 234
Db 121 APASGGECPAGGPVCKCERBPFLVILKESHLINKYRTGQVNCAPCYQPSFSADERTF 180
Qy 235 A 235
Db 181 A 181

RESULT 13
US-60-213-170-237
; Sequence 237; Application US/60213170
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, ELLEN
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: CL000699
; CURRENT APPLICATION NUMBER: US/60/213,170
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 678
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 237
; LENGTH: 232
; TYPE: PRT
; FEATURE:
; ORGANISM: HUMAN
; NAME/KEY: VARIANT
; LOCATION: (1)..(232)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-60-213-170-237

Query Match 77.4%; Score 1014; DB 27; Length 232;
Best Local Similarity 98.3%; Pred. No. 6.2e-77; 1; Indels 0; Gaps 0;
Matches 1/8; Conservative

Qy 55 FNHHTQDEAGLEVTHQFWPVIEIQSSPDLRFLFLCTMYTPICLDPYHKPLPPCRSVCEAKA 114
Db 1 FNHHTQDEAGLEVTHQFWPVIEIQSSPDLRFLFLCTMYTPICLDPYHKPLPPCRSVCEAKA 60
Qy 115 GCSPLMROQGFAWPERMSCDRLPVGDAEVLCMDYNRSSEATTAPRPRPAKPTLPGPGC 174
Db 61 GCSPLVLRQFGFAPWERMSCDRLPVGDAEVLCMDYNRSSEATTAPRPRPAKPTLPGPGC 120
Qy 175 APASGGECPAGGPVCKCERBPFLVILKESHLINKYRTGQVNCAPCYQPSFSADERTF 234
Db 121 APASGGECPAGGPVCKCERBPFLVILKESHLINKYRTGQVNCAPCYQPSFSADERTF 180
Qy 235 A 235
Db 181 A 181

RESULT 14
US-60-177-646-3449
; Sequence 3449; Application US/60177646
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, vivien
; TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
; FILE REFERENCE: CL000210
; CURRENT APPLICATION NUMBER: US/60/177,646
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 4226
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 3449
; LENGTH: 203
; TYPE: PRT

Query Match 70.2%; Score 920; DB 27; Length 203;
Best Local Similarity 99.4%; Pred. No. 4.5e-69; 1; Mismatches 0; Indels 0; Gaps 0;
Matches 1/62; Conservative

Qy 73 LVEIQCSDPLRFLCTMYTPICLDPYHKPLPPCRSVCEAKAGCSPLMROQGFAWPERMS 132
Db 1 LVEIQCSDPLRFLCTMYTPICLDPYHKPLPPCRSVCEAKAGCSPLMROQGFAWPERMS 60
Qy 133 CDRLPVIGDAEVLCMDYNRSSEATTAPRPRPAKPTLPGPGCAGSGECPCAGGPVCKC 192
Db 61 CDRLPVIGDAEVLCMDYNRSSEATTAPRPRPAKPTLPGPGCAGSGECPCAGGPVCKC 120
Qy 193 REPFPVIKESHLINKYRTGQVNCAPCYQPSFSADERTF 235
Db 121 REPFPVIKESHLINKYRTGQVNCAPCYQPSFSADERTF 163

Search completed: May 19, 2003, 16:41:30
Job time : 326 secs

GenCore version 5.1.4_P5_4578
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protein - protein search, using sw model

on on:

May 19, 2003, 16:34:42 ; Search time 90 Seconds
(w/o alignment)
455.046 Million cell updates/sec

title:
sequence:
effect score:
US-09-847-102A-68
1 MRRDPDRPPSLLLRLQI.....PNCAVPCVQPSFSDERIFPA 235

oring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5
797317 seqs, 17427795 residues

atched:
797317 seqs, 17427795 residues

total number of hits satisfying chosen parameters: 797317

minimum DB seq length: 0
maximum DB seq length: 200000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

No.	Score	Query Match Length	DB ID	Description
1	1310	100	585	US-10-01-764-9
2	1310	100	585	US-10-205-976-47
3	1300	99	233	US-10-264-825-35
4	824	62	694	US-10-311-623-6
5	824	62	694	US-10-285-976-53
6	824	62	694	US-10-115-678-250
7	824	62	694	US-10-112-944-250
8	824	62	694	US-10-452-680-21108
9	823.5	62	685	US-10-301-764-14
10	818	62	694	US-10-264-825-38
11	477	36	655	US-10-301-764-8
12	477	36	655	US-10-225-567A-382
13	477	36	565	US-10-285-976-41
14	472.5	36	563	US-10-60-53-139-9598
15	472.5	36	563	US-10-453-020-9598
16	469	35	818	US-10-264-825-32
17	461	35	574	US-10-385-976-51
18	448	34	251	US-10-264-825-37
19	440	33	572	US-10-01-764-13
20	415	31	647	US-10-205-976-39
21	412.5	31	518	US-10-264-825-31
22	412.5	30	591	US-10-285-976-55
23	393	30	229	US-10-264-825-39
24	388	29	597	US-10-017-165-800
25	384	29	225	US-10-454-825-40
26	29.3	6	581	US-10-285-976-57

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1	US-10-301-764-9
Sequence 9, Application US/10301764	
GENERAL INFORMATION:	
APPLICANT: Umansky, Samuel Melkonyan, Rovsep	
TITLE OF INVENTION: A FAMILY OF GENES ENCODING APOTOPSIS-RELATED PEPTIDES; PEPTIDES ENCODED THERAPY ANTI-CANCER AGENTS	
METHODS OF USE THEREOF	
NUMBER OF SEQUENCES: 19	
CORRESPONDENCE ADDRESS:	
ADDRESSEE: MORRISON & FERSTER	
STREET: 755 Page Mill Road	
CITY: Palo Alto	
STATE: CA	
COUNTRY: USA	
ZIP: 94304-1018	
COMPUTER READABLE FORM:	
MEDIUM TYPE: FLOPPY DISK	
COMPUTER: IBM PC compatible	
OPERATING SYSTEM: PC-DOS/MS-DOS	
SOFTWARE: Patentin Release #1.0, Version #1.30	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/10/301,764	
FILING DATE: 20-NOV-2002	
CLASSIFICATION: <Unknown>	
PRIORITY APPLICATION DATA:	
APPLICATION NUMBER: US/08/937,067	
FILING DATE: <Unknown>	
ATTORNEY/AGENT INFORMATION:	
NAME: Lehnhardt, Susan K.	
REGISTRATION NUMBER: 33,943	
REFERENCE/DOCKET NUMBER: 23647-20018.00	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: (650) 813-5660	
TELEX/FAX: (650) 494-0792	
INFORMATION FOR SEQ ID NO: 9:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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TOPOLOGY: linear	
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TOPOLOGY: linear	
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TOPOLOGY: linear	
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LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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LENGTH: 585 amino acids	
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TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
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SEQUENCE CHARACTERISTICS:	
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LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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SEQUENCE CHARACTERISTICS:	
LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
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LENGTH: 585 amino acids	
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STRANDEDNESS: single	
TOPOLOGY: linear	
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STRANDEDNESS: single	
TOPOLOGY: linear	
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TOPOLOGY: linear	
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LENGTH: 585 amino acids	
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TOPOLOGY: linear	
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TOPOLOGY: linear	
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LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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SEQUENCE CHARACTERISTICS:	
LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
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TOPOLOGY: linear	
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LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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SEQUENCE CHARACTERISTICS:	
LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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LENGTH: 585 amino acids	
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STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
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TOPOLOGY: linear	
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LENGTH: 585 amino acids	
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STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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LENGTH: 585 amino acids	
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STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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LENGTH: 585 amino acids	
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STRANDEDNESS: single	
TOPOLOGY: linear	
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LENGTH: 585 amino acids	
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STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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SEQUENCE CHARACTERISTICS:	
LENGTH: 585 amino acids	
TYPE: amino acid	
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TOPOLOGY: linear	
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STRANDEDNESS: single	
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STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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SEQUENCE CHARACTERISTICS:	
LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
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LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: Peptide	
SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 585 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE	

QY 1 MARPDPSAPSLILLALQVGRAMAAASKAPVCQEITVPMCRGIGYNLTMPNQFNHTQ 60
; APPLICANT: He, Biao
; APPLICANT: You, Liang
Db 1 MARPDPSAPSLILLALQVGRAMAAASKAPVCQEITVPMCRGIGYNLTMPNQFNHTQ 60
; APPLICANT: Xu, Zhidong
; APPLICANT: Jablons, David M.
QY 61 DEAGLEVHOFWPLVLEIQCSPDLRFLFLCTMVTICLPICLPYHKPLPPCRSVCEERAKAGCSPLM 120
; TITLE OF INVENTION: Methods for Treating Cancer by Inhibiting Wnt Signalling
; FILE REFERENCE: 023070-125601US
; CURRENT APPLICATION NUMBER: US/10/264,825
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PastSeq For Windows Version 3.0
Db 61 DEAGLEVHOFWPLVLEIQCSPDLRFLFLCTMVTICLPICLPYHKPLPPCRSVCEERAKAGCSPLM 120
QY 121 RQGFIAWERMSCDRPLVGRDAEVLCMDYNSSEATAPPRPFPAKPTLPGPGAPASGG 180
; SEQ ID NO: 35
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(233)
; OTHER INFORMATION: human Frizzled-5 peptide sequence
US-10-285-976-47
; US-10-264-825-35
; Sequence 47, Application US/10285976
; GENERAL INFORMATION:
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Corr, Maripat
; APPLICANT: Malini, Sen
; APPLICANT: Wu, Christina
; APPLICANT: Leoni, Lorenzo M.
; APPLICANT: Carson, Dennis A.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
; FILE REFERENCE: 023070-130320US
; CURRENT APPLICATION NUMBER: US/10/285,976
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 6/1287,995
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: WO PCT/US02/13802
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 47
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human frizzleds (Fzds)
US-10-205-976-47
; Sequence 47, Application US/10205976
; GENERAL INFORMATION:
; APPLICANT: Best Local Similarity 100.0%; Score 1310; DB 6; Length 233;
; Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
; APPLICANT: KALLICK, Deborah A.; TRIBOLEY, Catherine M.
; APPLICANT: YUE, Henry; NGUYEN, Daniel B.
; APPLICANT: TANG, Y. Tom; LAT, Preeti G.
; APPLICANT: POLICKY, Jennifer L.; AZIMMAI, Valda
; APPLICANT: LU, Duying; AINA M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HAFALIA, April J. A.; BAUGH, Mariah R.
; APPLICANT: BANDMAN, Olca; ARIVUZ, Chandra S.
; APPLICANT: YANG, Junming; XU, Yunling
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SAMANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brenda M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PF-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; RESULT 3
; Sequence 35, Application US/10264825
; GENERAL INFORMATION:

SEQ ID NO 6 LENGTH: 594
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No: 153444CD1
 US-10-311-623-6

Query Match 62.9%; Score 824; DB 6; Length 694;
 Best Local Similarity 59.9%; Pred. No. 5.2e-54; Mismatches 39; Indels 48; Gaps 8;
 Matches 161; Conservative 21; MisMatches 39; Indexes 48; Gaps 8;

Qy 11 SLL-LILLALQVLGRAMAASKAPVCOITVPMCRGIGNLTHMPNQHDTDEAGLEVH 68
 Db 11 SLL-LILLALQVLGRAMAASKAPVCOITVPMCRGIGNLTHMPNQHDTDEAGLEVH 70

Qy 69 QFWPLVEIQCSPDLPFLRFLCTMTPICLDPYKPLPPCRSVCERAKAGCAPLMRQYGAWP 128
 Db 71 QFWPLVEIQCSPDLPFLRFLCTMTPICLDPYKPLPPCRSVCERAKAGCAPLMRQYGAWP 130

Qy 129 ERMSCDRLPVLGRDAEVLCMDYNRSEATTA--PPRPFPAKPTLPG-----PPG 174
 Db 131 DRMRCDRLEQG-NPDTLMDYNRTDLTAAAPSPPRLPPPP--PGSQPSGSQHGRPPG 187

Qy 175 A-----PASGG-----ECPAGGFV---CKCREPFVILKSHP 205
 Db 188 ARPPHRGGGGGGDAAPPARGGGGKARPPGGGAAPCBPGCOCRAPMVSSSBRHP 247

Qy 206 LYNKVRTGQVPNCAPCVQYQPSASADERTF 234
 Db 248 LYNVKTGQIANCALPCPNPFSQDERAF 276

RESULT 5 US-10-2855-976-53

; Sequence 53, Application US/102855976
 ; GENERAL INFORMATION:
 ; APPLICANT: Rhie, Chae-Seo
 ; APPLICANT: Malini, Sen
 ; APPLICANT: Wu, Christina
 ; APPLICANT: Leoni, Lorenzo M.
 ; APPLICANT: Corr, Maripat
 ; APPLICANT: Carson, Dennis A.
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
 ; TITLE OF INVENTION: In Head and Neck Squamous Cell Carcinomas
 ; FILE REFERENCE: 023070-130320US
 ; CURRENT APPLICATION NUMBER: US/10/2855-976
 ; CURRENT FILING DATE: 2002-11-01
 ; PRIOR APPLICATION NUMBER: US 60/287,995
 ; PRIOR FILING DATE: 2001-05-01
 ; PRIOR APPLICATION NUMBER: WO PCT/US02/13802.
 ; NUMBER OF SEQ ID NOS: 232
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 53
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human frizzled8 (Fz8B)
 ; US-10-2855-976-53

Query Match 62.9%; Score 824; DB 6; Length 694;
 Best Local Similarity 59.9%; Pred. No. 5.2e-54; Mismatches 39; Indels 48; Gaps 8;
 Matches 161; Conservative 21; MisMatches 39; Indexes 48; Gaps 8;

Qy 11 SLL-LILLALQVLGRAMAASKAPVCOITVPMCRGIGNLTHMPNQHDTDEAGLEVH 68
 Db 11 SLL-LILLALQVLGRAMAASKAPVCOITVPMCRGIGNLTHMPNQHDTDEAGLEVH 70

Qy 69 QFWPLVEIQCSPDLPFLRFLCTMTPICLDPYKPLPPCRSVCERAKAGCAPLMRQYGAWP 128
 Db 71 QFWPLVEIQCSPDLPFLRFLCTMTPICLDPYKPLPPCRSVCERAKAGCAPLMRQYGAWP 130

Qy 129 ERMSCDRLPVLGRDAEVLCMDYNRSEATTA--PPRPFPAKPTLPG-----PPG 174
 Db 131 DRMRCDRLEQG-NPDTLMDYNRTDLTAAAPSPPRLPPPP--PGSQPSGSQHGRPPG 187

Qy 175 A-----PASGG-----ECPAGGFV---CKCREPFVILKSHP 205
 Db 188 ARPPHRGGGGGGDAAPPARGGGGKARPPGGGAAPCBPGCOCRAPMVSSSBRHP 247

Qy 206 LYNKVRTGQVPNCAPCVQYQPSASADERTF 234
 Db 248 LYNVKTGQIANCALPCPNPFSQDERAF 276

RESULT 6 US-10-115-678-250

; Sequence 250, Application US/10115678
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Wang, Gezhi
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Ghosh, Malabika
 ; APPLICANT: Wang, Dunru
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Wang, Zhiwei
 ; TITLE OF INVENTION: Novel Nucleic Acids and
 ; TITLE OF INVENTION: Secreted Polypeptides
 ; FILE REFERENCE: 803ACON
 ; CURRENT APPLICATION NUMBER: US/10/115,678
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 10/112,944
 ; PRIOR FILING DATE: 2002-03-28
 ; PRIOR APPLICATION NUMBER: US 60/306,971
 ; PRIOR FILING DATE: 2001-07-21
 ; PRIOR APPLICATION NUMBER: US 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: US 09/991,404
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: US 09/496,914
 ; PRIOR FILING DATE: 2000-02-03
 ; PRIOR APPLICATION NUMBER: US 09/515,126
 ; PRIOR FILING DATE: 2000-02-28
 ; PRIOR APPLICATION NUMBER: US 09/519,705
 ; PRIOR FILING DATE: 2000-03-07
 ; PRIOR APPLICATION NUMBER: US 09/440,217
 ; PRIOR FILING DATE: 2000-03-31
 ; PRIOR APPLICATION NUMBER: US 09/552,929
 ; PRIOR FILING DATE: 2000-04-18
 ; PRIOR APPLICATION NUMBER: US 09/577,408
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 924
 ; SOFTWARE: pt_Fl_genes Version 5.0
 ; SEQ ID NO 250
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-115-678-250

Query Match 62.9%; Score 824; DB 6; Length 694;
 Best Local Similarity 59.9%; Pred. No. 5.2e-54; Mismatches 39; Indels 48; Gaps 8;
 Matches 161; Conservative 21; MisMatches 39; Indexes 48; Gaps 8;

Qy 11 SLL-LILLALQVLGRAMAASKAPVCOITVPMCRGIGNLTHMPNQHDTDEAGLEVH 68
 Db 11 SLL-LILLALQVLGRAMAASKAPVCOITVPMCRGIGNLTHMPNQHDTDEAGLEVH 70

QY 69 QFWLVEIQCSPDPLRFCLMVTICLPLDVKPKPCRSVCRAKAGCSPLMROYGFAMP 128
Db 71 QFWLVEIQCSPDPLKFLCSMVTPICTEDYKKLPVCRSVCRAKAGCSPLMROYGFAMP 130
QY 129 ERMSCDRLPVLGDRAEVLCDMDYNESEATTA--PPRPFPAKPTLPG-----PPG 174
Db 131 DRMCDRLPDQEKG-NPDTLCMDYNTDLTTAAPSPPRLPPP--PGQOPPSGSGHGRPG 187
QY 175 A-----PASGG----ECPPAGGPV---CKCREPFVILKESHP 205
Db 175 A-----PASGG----ECPPAGGPV---CKCREPFVILKESHP 205
QY 188 ARPPHRGGGGGDAAAPARGGGGKARPQQGGAAAPCEPGCOCRAPMVSSEHP 247
Db 206 LYNKVRTGQVNCAPVCYQPSFSADERIF 234
QY 248 LYNKVRTGQVNCALPCNPPFSQDERAF 276

RESULT 7 US-10-112-944-250

; Sequence 250, Application US/10112944
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom.
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feivan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei

TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 805A

CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: ptc_FL_genes Version 5.0
SEQ ID NO: 250
LENGTH: 694
TYPE: PRT
ORGANISM: Homo sapiens
US-60-452-680-21108

Query Match 62.9%; Score 824; DB 7; Length 694;
Best Local Similarity 59.9%; Pred No. 5.2e-54;
Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;

QY 11 SLL--LILLAQLQVRAAAASKAVPQOEITVPMQRGIGNLTHMPQNQHIDTDEAGLEVH 68
Db 11 SLLAALALIQRRSSGAAASAKELACQETIVPLCKGIGNYTMQPNQHIDTDEAGLEVH 70

QY 69 QFWLVEIQCSPDPLRFCLMVTICLPLDVKPKPCRSVCRAKAGCSPLMROYGFAMP 128
Db 71 QFWLVEIQCSPDPLKFLCSMVTPICTEDYKKLPVCRSVCRAKAGCSPLMROYGFAMP 130
QY 129 ERMSCDRLPVLGDRAEVLCDMDYNESEATTA--PPRPFPAKPTLPG-----PPG 174
Db 131 DRMCDRLPDQEKG-NPDTLCMDYNTDLTTAAPSPPRLPPP--PGQOPPSGSGHGRPG 187
QY 175 A-----PASGG----ECPPAGGPV---CKCREPFVILKESHP 205
Db 175 A-----PASGG----ECPPAGGPV---CKCREPFVILKESHP 205
QY 188 ARPPHRGGGGGDAAAPARGGGGKARPQQGGAAAPCEPGCOCRAPMVSSEHP 247
Db 206 LYNKVRTGQVNCAPVCYQPSFSADERIF 234
QY 248 LYNKVRTGQVNCALPCNPPFSQDERAF 276

RESULT 8 US-60-452-680-21108

; Sequence 21108, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michael
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL01450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SBO ID NO: 21108
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-21108

Query Match 62.9%; Score 824; DB 7; Length 694;
Best Local Similarity 59.9%; Pred No. 5.2e-54;
Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;

QY 11 SLL--LILLAQLQVRAAAASKAVPQOEITVPMQRGIGNLTHMPQNQHIDTDEAGLEVH 68
Db 11 SLLAALALIQRRSSGAAASAKELACQETIVPLCKGIGNYTMQPNQHIDTDEAGLEVH 70

QY 69 QFWLVEIQCSPDPLRFCLMVTICLPLDVKPKPCRSVCRAKAGCSPLMROYGFAMP 128
Db 71 QFWLVEIQCSPDPLKFLCSMVTPICTEDYKKLPVCRSVCRAKAGCSPLMROYGFAMP 130
QY 129 ERMSCDRLPVLGDRAEVLCDMDYNESEATTA--PPRPFPAKPTLPG-----PPG 174
Db 131 DRMCDRLPDQEKG-NPDTLCMDYNTDLTTAAPSPPRLPPP--PGQOPPSGSGHGRPG 187
QY 175 A-----PASGG----ECPPAGGPV---CKCREPFVILKESHP 205
Db 175 A-----PASGG----ECPPAGGPV---CKCREPFVILKESHP 205
QY 188 ARPPHRGGGGGDAAAPARGGGGKARPQQGGAAAPCEPGCOCRAPMVSSEHP 247
Db 206 LYNKVRTGQVNCAPVCYQPSFSADERIF 234
QY 248 LYNKVRTGQVNCALPCNPPFSQDERAF 276

RESULT 9 US-10-301-764-14

; Sequence 14, Application US/10301764
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuil
; Meikonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; APOTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; NUMBER OF SEQUENCES 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA

COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,764
FILING DATE: 20-Nov-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 685 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-301-764-14

Query Match Best Local Similarity Score DB Length
Matches 60.0%; Pred. No. 5.6e-54; 823.5; 6; 685;
Matched 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;

Qy 11 SLL--LILQLAQLVGRAAASKAPVCOELTPMRCIGNLTHMPNQFHDTDEAGLEVH 68
Db 11 SLLAALAILQRLQSSGAAAKSAKELACOBITVPLCKGIGNYTYPNQFHDTDEAGLEVH 70
Qy 69 QFWPLVEIQCSPDLRFFLCTMYTPICLPDYHKELPPRSVCERAKGSPSLMRQYGFAMP 128
Db 71 QFWPLVEIQCSPDLKFLCSWYTPICEDYKRLPPRSVCERAKGCAPLMRQYGFAMP 130
Qy 129 ERMSCDRLPVLSRDAEVLMCDMDYNRSEATTA--PPRPFPAKPTLPG-----PPG 174
Db 131 DRMRCDRLPEQG-NPDTLCMDYNRTDLTTAAPSPPRRLLPPP--PGEOPPSGSGHGRPPG 187
Qy 175 A-----PASGG-----ECPPGGPV---KCRCBPFPVILKESHP 205
Db 188 ARPRPHGGRRGGGGAAAPPARGGGGGKARPPGGGAAPCEPGCCQCRAPMVSVSERHP 247
Qy 206 LYKVKRTQGVNPNCAPVCPYQPSFSADER 232
Db 248 LYNRKTKIQIANGALPCINPFFSODER 274

RESULT 10
US-10-264-825-38
Sequence 38, Application US/10264825
GENERAL INFORMATION:
APPLICANT: He, Biao
APPLICANT: You, Liang
APPLICANT: Xu, Zhidong
APPLICANT: Jablons, David M.
TITLE OF INVENTION: Methods for Treating Cancer by
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/264,825
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 38
LENGTH: 275

RESULT 11
US-10-301-764-8
Sequence 8, Application US/10301764
GENERAL INFORMATION:
APPLICANT: Umansky, Samuel
APPLICANT: Melkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
APOTOTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,764
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 amino acids
TYPE: amino acid

US-10-264-825-38
Query Match Best Local Similarity Score DB Length
Matches 59.9%; Pred. No. 6.7e-54; 818; 6; 275;
Matched 160; Conservative 21; Mismatches 38; Indels 48; Gaps 8;

Qy 11 SLL--LILQLAQLVGRAAASKAPVCOELTPMRCIGNLTHMPNQFHDTDEAGLEVH 68
Db 11 SLLAALAILQRLQSSGAAAKSAKELACOBITVPLCKGIGNYTYPNQFHDTDEAGLEVH 70
Qy 69 QFWPLVEIQCSPDLRFFLCTMYTPICLPDYHKELPPRSVCERAKGSPSLMRQYGFAMP 128
Db 71 QFWPLVEIQCSPDLKFLCSWYTPICEDYKRLPPRSVCERAKGCAPLMRQYGFAMP 130
Qy 129 ERMSCDRLPVLSRDAEVLMCDMDYNRSEATTA--PPRPFPAKPTLPG-----PPG 174
Db 131 DRMRCDRLPEQG-NPDTLCMDYNRTDLTTAAPSPPRRLLPPP--PGEOPPSGSGHGRPPG 187
Qy 175 A-----PASGG-----ECPPGGPV---KCRCBPFPVILKESHP 205
Db 188 ARPRPHGGRRGGGGAAAPPARGGGGGKARPPGGGAAPCEPGCCQCRAPMVSVSERHP 247
Qy 206 LYKVKRTQGVNPNCAPVCPYQPSFSADER 232
Db 248 LYNRKTKIQIANGALPCINPFFSODER 274

STRANDEDNESS: single
TOPOLogy: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8

US-10-301-764-8

Query Match 36.4%; Score 477; DB 6; Length 565;
Best Local Similarity 41.9%; Pred. No. 4.8e-28; Gaps 11;
Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

Qy 3 RPDPSAPPSSLLLAQVLGRAAAASKAPV-----COEITVPMCRGIGYNLTHMPNQF 55
Db 2 RPRSLALRLLLPLLAQVLGRAAAASKAPV-----COEITVPMCRGIGYNLTHMPNQF 55

Qy 56 NHDTQDEAGLEVHQFWPLVEIQCSPDPLRFLLCTMYTPICLPDYHKPLPCCRSCYERAKAG 115
Db 62 GHTNQEDAGLEVHQFYPLVKVQCSPELRFLCSMYPVCTV-LEQAIIPCRSICERARQG 120

Qy 169 LPGPPGAPASGGCPCAGG---PFVCKCREPFVPLKESHLPLYNKVRGQVNPACVQYQ 224
Db 176 AGGTPGCPGGGAPPRYATLEHFPHC-----RVLKV--PSVLSYKELGERDCAAPC-E 226

Qy 225 PS-----FSADERTFA 235
Db 227 PARPDGSMFFSOETRFA 244

RESULT 12

; Sequence 382, Application US/10225567A
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Gleena C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2392
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 382
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-225-567A-382

Query Match 36.4%; Score 477; DB 6; Length 565;
Best Local Similarity 41.9%; Pred. No. 4.8e-28; Gaps 11;
Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

Qy 3 RPDPSAPPSSLLLAQVLGRAAAASKAPV-----COEITVPMCRGIGYNLTHMPNQF 55
Db 2 RPRSLALRLLLPLLAQVLGRAAAASKAPV-----COEITVPMCRGIGYNLTHMPNQF 55

Qy 56 NHDTQDEAGLEVHQFWPLVEIQCSPDPLRFLLCTMYTPICLPDYHKPLPCCRSCYERAKAG 115
Db 62 GHTNQEDAGLEVHQFYPLVKVQCSPELRFLCSMYPVCTV-LEQAIIPCRSICERARQG 120

Qy 169 LPGPPGAPASGGCPCAGG---PFVCKCREPFVPLKESHLPLYNKVRGQVNPACVQYQ 224
Db 176 AGGTPGCPGGGAPPRYATLEHFPHC-----RVLKV--PSVLSYKELGERDCAAPC-E 226

Qy 225 PS-----FSADERTFA 235
Db 227 PARPDGSMFFSOETRFA 244

RESULT 13

US-10-285-976-41

; Sequence 41, Application US/10285976
; GENERAL INFORMATION:
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Malini, Sen
; APPLICANT: Wu, Christina
; APPLICANT: Leoni, Lorenzo M.
; APPLICANT: Corr, Maripat
; APPLICANT: Carson, Dennis A.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
; FILE REFERENCE: 02/070-13032015
; CURRENT APPLICATION NUMBER: US/10/285,976
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/287,995
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: WO PCT/US02/13802
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human frizzled2 (Frz2)

US-10-285-976-41

Query Match 36.4%; Score 477; DB 6; Length 565;
Best Local Similarity 41.9%; Pred. No. 4.8e-28; Gaps 11;
Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

Qy 3 RPDPSAPPSSLLLAQVLGRAAAASKAPV-----COEITVPMCRGIGYNLTHMPNQF 55
Db 2 RPRSLALRLLLPLLAQVLGRAAAASKAPV-----COEITVPMCRGIGYNLTHMPNQF 55

Qy 56 NHDTQDEAGLEVHQFWPLVEIQCSPDPLRFLLCTMYTPICLPDYHKPLPCCRSCYERAKAG 115
Db 62 GHTNQEDAGLEVHQFYPLVKVQCSPELRFLCSMYPVCTV-LEQAIIPCRSICERARQG 120

Qy 169 LPGPPGAPASGGCPCAGG---PFVCKCREPFVPLKESHLPLYNKVRGQVNPACVQYQ 224
Db 176 AGGTPGCPGGGAPPRYATLEHFPHC-----RVLKV--PSVLSYKELGERDCAAPC-E 226

Qy 225 PS-----FSADERTFA 235
Db 227 PARPDGSMFFSOETRFA 244

RESULT 14

US-60-453-135-959B

; Sequence 958, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Iakoubova, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL01456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762

; SEQ ID NO: 9598
; LENGTH: 563
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-9598

Search completed: May 19, 2003, 16:43:09
Job time : 94 secs

Query Match 36.1%; Score 472.5; DB 7; Length 563;
Best Local Similarity 42.7%; Pred. No. 1.1e-27;
Matches 109; Conservative 30; Mismatches 75; Indels 41; Gaps 12;
Qy 7 SAPPSILL-LLAQVNGRAAAASKPV-----CQEITVPMCRGIGIYUITHMPNQFNHD 58
Db 3 SALPRILLPLILLPRAAGPQFNGKISIPDHGFCQPISPICLTDIAVQNTMNLGTT 62
Qy 59 TQEAGLEPHQFWPIVEIQCSPDILRFFLCTMWYTPCLPDYHKPLPCKRSVCERAKAGSP 118
Db 63 NQEDGLEVHQFYFLVKVQCSPELRFFLCSMAYPCVTV-LEQAIIPCRSICERAKQGCB 121
Qy 119 LMRQYGFAMPERMCDRLPVLGRADAEVLCDMDNSE-----ATTAPRPFPA-KPTLPG 171
Db 122 LMNRKGFPWPERLRCHEFPRHG--AEQICVGQNHSEDGAPALLTAPP---PGLQPGAGG 176
Qy 172 PPGPASPBCPAGGG----PFVCKCREPFVPIIKESSHPLYNKVITQVNCAVCCYQPS- 226
Db 177 TPGGBGGGAPPRVATLEHPFHCP-----RVLKV--PSYLSYKFLGERDCAAAPC-EPAR 227
Qy 227 -----FSADERTA 235
Db 228 PDGSNFFSQBETRFA 242

RESULT 15

US-60-453-050-9598

; Sequence 9598, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele

APPLICANT: LUKE, May
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CL001457

CURRENT APPLICATION NUMBER: US/60/453, 050
CURRENT FILING DATE: 2003-03-10

NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 9598

LENGTH: 563
TYPE: PRT
ORGANISM: Homo sapiens

US-60-453-050-9598

Query Match 36.1%; Score 472.5; DB 7; Length 563;
Best Local Similarity 42.7%; Pred. No. 1.1e-27;
Matches 109; Conservative 30; Mismatches 75; Indels 41; Gaps 12;

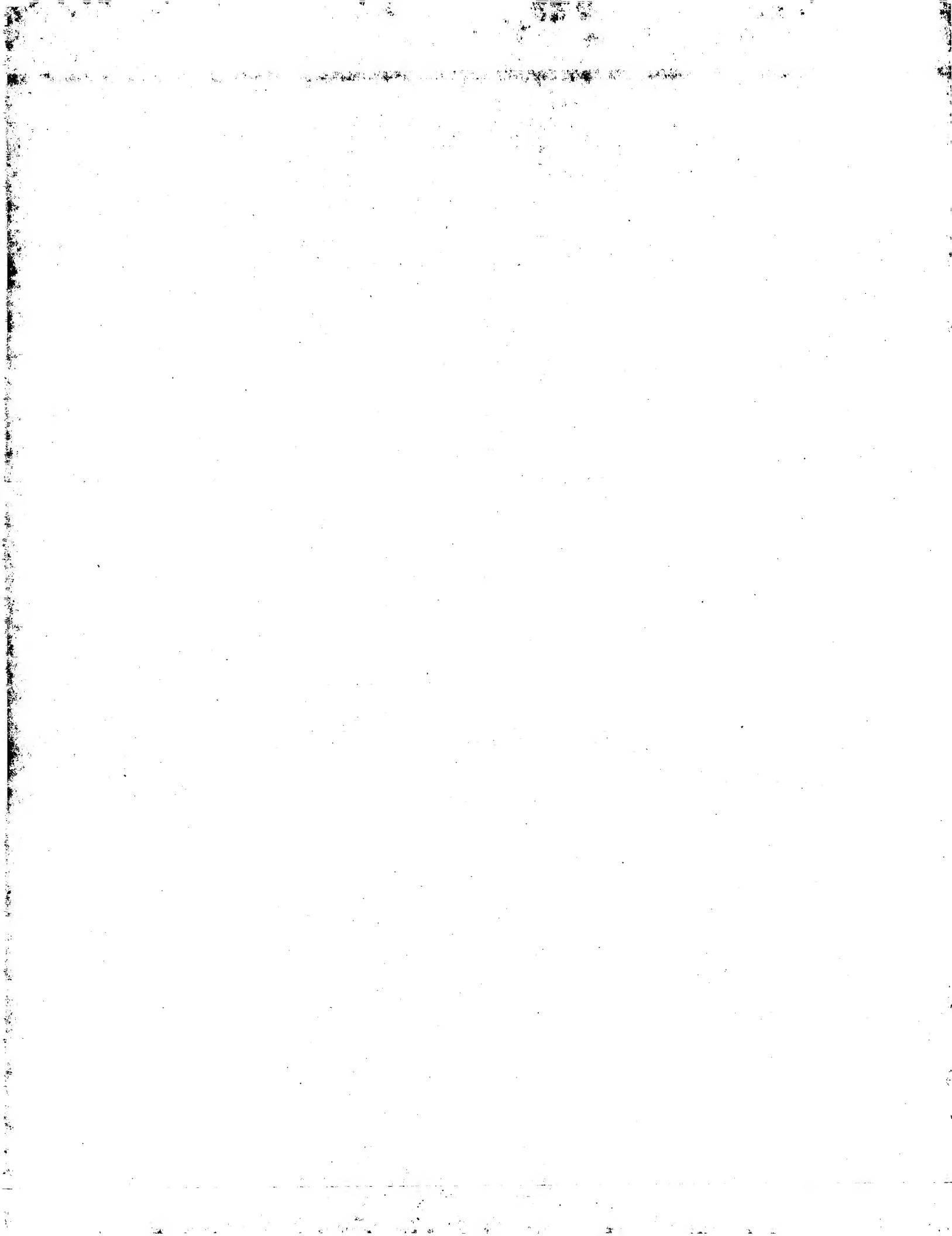
Qy 7 SAPPSILL-LLAQVNGRAAAASKPV-----CQEITVPMCRGIGIYUITHMPNQFNHD 58
Db 3 SALPRILLPLILLPRAAGPQFNGKISIPDHGFCQPISPICLTDIAVQNTMNLGTT 62

Qy 59 TQEAGLEPHQFWPIVEIQCSPDILRFFLCTMWYTPCLPDYHKPLPCKRSVCERAKAGSP 118
Db 63 NQEDGLEVHQFYFLVKVQCSPELRFFLCSMAYPCVTV-LEQAIIPCRSICERAKQGCB 121

Qy 119 LMRQYGFAMPERMCDRLPVLGRADAEVLCDMDNSE-----ATTAPRPFPA-KPTLPG 171
Db 122 LMNRKGFPWPERLRCHEFPRHG--AEQICVGQNHSEDGAPALLTAPP---PGLQPGAGG 176

Qy 172 PPGPASPBCPAGGG----PFVCKCREPFVPIIKESSHPLYNKVITQVNCAVCCYQPS- 226
Db 177 TPGGBGGGAPPRVATLEHPFHCP-----RVLKV--PSYLSYKFLGERDCAAAPC-EPAR 227

Qy 227 -----FSADERTA 235
Db 228 PDGSNFFSQBETRFA 242



GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on:

May 22, 2003, 21:14:04 ; Search time 2410 Seconds
 (without alignments)

2451.653 Million cell updates/sec

Title: US-09-847-102a-68
 Perfect score: 1310
 Sequence: 1 MARPDPSAPPSSULLLQL.....PNCAVPCYQPSFSADERTFA 235

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 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 DelOp .6.0 , Delect 7.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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 -DB_PENDING_Patents_NA_Main -OFMT=fastap -SUFFIX=rimp -MINMATCH=0.1 -LOOPCL=0
 -LOOPEXT=0 -UNITS=bts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cgi
 -LIST=45 -DOCALLER=200 -THR SCORE_PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
 -MODER=LOCAL -OUTFILE=PTO -NORMEXT -HEAPSIZE=00 -MINLEN=0 -MAXLEN=200000000
 -USER=US09847102 @CCN 1 1 2950 @runat 19052003 160408 762 -NCPU=6 -ICPU=3
 -NO_NMAP -LARGEQ2 -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA_Main,*

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 2: /cgn2_6/prodata/1/pna/US61_COMB.seq: *
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 5: /cgn2_6/prodata/1/pna/US81_COMB.seq: *
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 23: /cgn2_6/prodata/1/pna/US96B_COMB.seq: *
 24: /cgn2_6/prodata/1/pna/US96C_COMB.seq: *
 25: /cgn2_6/prodata/1/pna/US96D_COMB.seq: *
 26: /cgn2_6/prodata/1/pna/US96E_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1310	100.0	2334	12 US-09-832-340-9	Sequence 9, Appl
2	1310	100.0	2334	14 US-09-053-375B-1495	Sequence 1495, Appl
3	1310	100.0	2334	15 US-09-107-112-3	Sequence 3, Appl
4	1310	100.0	2334	41 US-10-152-548-9	Sequence 9, Appl
5	1310	100.0	2334	45 US-60-105-307-9	Sequence 9, Appl
6	1306	99.7	3124	64 US-60-207-360-77	Sequence 77, Appl

SEQUENCE DESCRIPTION: SEQ ID NO: 9: (frizzled 5) mRNA, Coding region: 321...2078

US-10-152-548-9

Alignment Scores: 2.01e-73 Length: 2334

Score: 1.10.00 Matches: 235

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: Gaps: 0

RESULT 4

US-10-152-548-9

Sequence 9, Application US/10152548

GENERAL INFORMATION:

APPLICANT: Bhanot, Purnima

Brink, Marcel

Haiyman, Cindy S.

Wang, Yanshu

Hsieh, Jen-chih

Andrew, Deborah

Nathans, Jeremy

TITLE OF INVENTION: Wnt Receptor Compositions and Methods

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSE: Dehlinger & Associates

STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto

STATE: CA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/152,548

FILING DATE: 21-MAY-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/832,340

FILING DATE: 11-APR-1997

APPLICATION NUMBER: US 60/015,307

FILING DATE: 12-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615

REFERENCE/DOCKET NUMBER: 8600-0167-30

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0980

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 2334 base pairs

TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Human transmembrane receptor

741 CGCGACGCCGAGGTCCTGTGATGATTACAACGGAGGCCACCGGGCCCCC 800

161 ArgProPheProLysProThrLeuProGlyProProGlyAlaProAlaSerGly 180

801 AGCCCTTCCACGCCAACCCACCTTCAGGGCCGCAAGGGCCACCTGGGGC 860

181 GluCysProAlaGlyGlyProPheValCysLySArgGluProPheValProLeu 200

861 GATGCCCGCTGGGGCCGTTGTGCAACTGTGGAGCCCTTGCTGCCATCTG 920

201 LysGlusRHisProLeuTyRasnLysValArgThrGlyGlnValProAsnCysAlaVal 220

921 AAGGAGTCACACCCGCTCTACACAAGTGCCGAGGCCACCTGGGGTA 980

221 ProCysTyrgInProSerPheserAlaaspGluArgThrPhala 235

981 CCCTGCTTACCGCCGTCCTCACTGCCCACGAGCACTGGTCCC 1025

381 GTGGCCGGGGGCGCCGCGCTCTATGCAATATGCAAGGCGCAACTGTGGCGCATG 440

41 CySArgGlyIleGlyTyRasnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60

441 TGCGCGGGCATCGCTACACCTCCGCACCGCCCTCGCTGCTGCTGCGACGCTG 380

61 AspGluAlaGlyIleGlyTyRasnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 20

501 GACGAGGGGGCATGGCTGACAGTCGACCAGTCCTACCGCTGCTGAGATCCAATCTCGCCG 566

81 AspLeuArgPhePheLeuCysThrMetTyrrProleCysLeuProAspTyRasnLys 1000

621 CGCTGCGCCCTCTCCGCTGCGCAAGGCCGCTGCTGCCCTGAG 6200

561 GACTGCGCTCTCTCTATGCAAGGCGCAACTGTGTGCCGACTACACAG 6000

121 ArgGluAlaGlyIleGluValHisGlnPheThrProLeuValGluGlyGlyCysSerPro 80

681 CGCCAGTAGGGCTTGGCTGGCCGAGGCGCATGAGCTGCGACGCCCTCGCTGGCTGGC 740

141 ArgSpaAlaGluValLeuCysMetAspTyRasnLysValGlyCysSerProLeuMet 1660

741 CGCGACGCCGAGGTCCTGTGATGATTACAACGGAGGCCACCGGGCCCCC 8600

161 ArgProPheProLysProThrLeuProGlyProProGlyAlaProAlaSerGly 180

801 AGCCCTTCCACGCCAACCCACCTTCAGGGCCGCAAGGGCCGCGCCCTGGGGC 866

181 GluCysProAlaGlyGlyProPheValCysLySArgGluProPheValProLeu 200

861 GATGCCCGCTGGGGCCGTTGTGCAACTGTGGAGCCCTTGCTGCCATCTG 920

201 LysGlusRHisProLeuTyRasnLysValArgThrGlyGlnValProAsnCysAlaVal 220

921 AAGGAGTCACACCCGCTCTACACAAGTGCCGAGGCCACCTGGGGTA 980

221 ProCysTyrgInProSerPheserAlaaspGluArgThrPhala 235

981 CCCTGCTTACCGCCGTCCTCACTGCCCACGAGCACTGGTCCC 1025

RESULT 5

US-60-015-307-9

Sequence 9, Application US/60015307

GENERAL INFORMATION:

APPLICANT: Bhanot, Purnima

Brink, Marcel

Haiyman, Cindy S.

Wang, Yanshu

Hsieh, Jen-chih

Andrew, Deborah

Nathans, Jeremy

```

QY 121 ArgGlnTygGlyPheAlaIrrppGluIrgMetSerCysAspBrgLauProAllelGly 140
Db 681 CGCCAGTACCGCTGGCTGGCTGGCCGAGGCCATGAGCTGGACGCCCTGGGCTGGC 740
QY 141 ArgApApaLgluValLeuGlyBmaAspTyrAspArgSerGluAlaThrAlaProPro 160
Db 741 CGCGAGGCCGAGGTCCTCTGCATGATTACAACCGCAGGCCACACGGGCC 800
QY 161 ArgProPheProAlaLysProThrLeuProGlyProProGlyAlaProAlaSerGly 180
Db 801 AGGCCTTCCCAGGCCACCTTCAGGCCGGCCAGGCCAGGGCCGGCG 860
QY 181 GluGlyProLalGlyGlyProPheValCysValGluProPheValProIleu 200
Db 861 GAATGCCCTCTGGGGCCGTTGTGTCGAAGTGTGTCGGAGGCCCTGGTGCCTTG 920
QY 201 LysGluSerHisProLeuTrpLysValArgThrGlyGlnValProAsnCysAlaVal 220
Db 921 AAGGGAGTCACACCCGCTCACACAAGGGCGGAGGCCAGGGCC 980
QY 221 ProGlyTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
Db 981 CCCCTCTTACCAAGCCGTCCTCAGGCCGAGCCAGCTCC 1025
US-60-207-360-77
; Sequence 77, Application US/60207360
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: CL000591
; CURRENT APPLICATION NUMBER: US/60/207,360
; CURRENT FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 77
; LENGTH: 3124
; TYPE: DNA
; ORGANISM: HUMAN
; US-60-207-360-77

Alignment Scores:
Pred. No.: 4.85e-73 Length: 3124
Score: 1306.00 Matches: 234
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.57%
Query Match: 99.69% Mismatch: 0
DB: 64 Indels: 0
Gaps: 0

US-09-847-102A-68 (1-235) x US-60-207-360-77 (1-3124)

QY 1 MetAlaLargProAlaProSerAlaProSerIeuLeuLeuLeuLeuLeuAlaGlnIeu 20
Db 547 ATGGTCGGCTGACCATCGGCCGCCCTCGCTGTTCTGCTGCTCTGGGAGCTG 606
QY 21 ValGlyArgAlaAlaAlaAlaSerTysAlaProValCysGlnIeuThrValProMet 40
Db 607 GTGCGCCGCGCCGCGCCGCGCCGTCAGGCCCCGGTGTCCAGGAAATACGGGCCATG 666
QY 41 CysArgGlyIleGlyTyrAlaLeuThrIleMetProAspGlnPheAsnHisAspTyrGln 60
Db 667 TGCCTCCGGCATCGGCCATCACACTGAGCACATGCCAACCGATCAACCAACGACAG 726
QY 61 AspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGluIleGlnCysSerPro 80
Db 727 GACGAGGCCGCGCTGGAGGTGACCCAGTCTGSCCCGCTGTGAGAGATCCAACTCTCGCG 786
QY 81 AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisLys 100
Db 787 GACCTGGCTCTCTCTATGCTCTATGACACGCCCATCTGCTGCGCCGACTACCAACAG 846

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QY 101 ProLeuProProCysArgSerValCysGluLysAlaGlyCysSerProLeuMet 120
Db 847 CGCTGGCCCGCCGCTGGTGCAGGGCCAGGGCGCTGGCTCGCGCTATG 906
QY 121 ArgGlnTyrglPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGly 140
Db 907 CCGCAGTAGCTTCGCTGGCCGAGCGATGAGCTGGCCCTCCCCTGGCG 966
QY 141 ArgGlnTyrglPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGly 140
Db 967 CGGACGCCGAGCTCTGATGGATTAACCGCGAGGAGCCACACGGCC 1026
QY 161 ArgProProPheProAlaLysProThrLeuProGlyProGlyAlaProAlaSerGly 180
Db 1027 AGCCCTTCCACCCAGCCACCTTCAGGCCGCCAGGGCGCTGGGGGG 1086
QY 181 GluCysProAlaGlyGlyProPheValCysLysCysArgLysCysLys 200
Db 1087 GATGCCCGCTGGGGCCGTTGGTGCGAAGTGTGGCTGGGGGG 1146
QY 201 LysGluSerHisProLeuProTyrosylValArgThrGlyLysValProAsnCysAlaVal 220
Db 1147 AGGAGTCACACCGCTCTAACACAAGTGCGGAGGCCAGTGCCCAACTGGGCGTA 1206
QY 221 ProCysTyrglProSerPheserAlaLysPheGluArgThrPheAla 235
Db 1207 CCTGTCTACCGCCGCTTCACTGCCCCAGAGCGCACGTTGCC 1251
RESULT 7
US-60-129-391-1913
Sequence 1913, Application US/60129391
GENERAL INFORMATION:
APPLICANT: Keith et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN THE DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: 10716-138
CURRENT FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 3674
SEQ ID NO 1913
LENGTH: 2555
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (1),(2552),(2553), (2554), (2555)
OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknc
US-60-129-391-1913
Alignment Scores:
Pred. No.: 6.13e-71 Length: 2555
Score: 1271.50 Matches: 232
Percent Similarity: 99.15% Conservative: 1
Best Local Similarity: 98.72% Mismatches: 1
Query Match: 97.06% Indels: 2
DB: 56 Gaps: 1
US-0-9-847-102A-68 (1-235) x US-60-129-391-1913 (1-2555)
QY 1 MetAlaArgProAspProSerAlaProProSerIleLeuLeuLeuLeuAlaGlnLeu 20
Db 383 ATGGCTGGCTCTGACCCATCCTGGCCGCGCTGGCTGGCTGGCGAGCTG 442
QY 21 ValGlyArgAlaAlaAlaAlaSerLysAlaProValCysGlnGluLeuThrValProMet 40
Db 443 GGGGCCGGGAGCCGCCGGTCAAGC-C--TCCAGAAATCAGGTCGCCATG 498
QY 41 CysArgGlyLysGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
Db 499 TCCGGCGCATCGCTACACCTGACGACATGCCAACGAGCAACGACACCGAG 558
QY 61 AspGluAlaGlyLeuGluAlaHisGlnPheProLeuValGluLeuGlnCysSerPro 80
Db 559 GACGAGCGGAGCCTGGAGGTCACCAAGTCTGGCCGCTGGGGAGATTCAAATGCTGGCC 618
QY 81 AspLeuArgPhePheLeuCysThrMetTYrThrProIleCysLeuProAspTYrHisLys 100
Db 619 GACCTGGCTCTTCATGCTCTGATCACGCCATCTGCTGCTCCCGACTAACAG 678
QY 101 ProLeuProProCysArgSerValCysGluArgAlaLysAlaGlyCysSerProLeuMet 120
Db 679 CGCTGGCCCTGCGCTCGCTGGAGGGGCCAGGGCGCTGCGCTGGCTGCGCTGATG 738
QY 121 ArgGlnTyrglPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGly 140
Db 739 CGCCAGTAGCTGGCTGGCCCTGGGGAGGAGCCATGAGCTGGAGCCCTCCCGTGCG 798
QY 141 ArgGlnTyrglPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGly 140
Db 799 CGCGAGCCGAGGTCCTCTGATGATTAACCGCGAGGCCACAGGGCC 858
QY 161 ArgProProPheProAlaLysProThrLeuProGlyAlaProAlaSerGly 180
Db 859 AGCCCTTCCACCCAGGCCACCTTCAGGCCGCCAGGGGCCAGGGGCCCTGGGGGG 918
QY 181 GluCysProAlaGlyGlyProPheValCysLysCysArgLysCysLys 200
Db 919 GATGCCCGCTGGGGCCGTCGTCAGTGTGCGAGCCCTGGGCCCTGGGCCCTG 978
QY 201 LysGluSerHisProLeuProTyrosylValArgThrGlyLysValProAsnCysAlaVal 220
Db 979 ANGAGTCACACCGCTCTAACACAAGTGCGGAGGCCACACTGCGCGTA 1038
QY 221 ProCysTyrglProSerPheserAlaLysPheGluArgThrPheAla 235
Db 1039 CCTGTCTACCGCCGCTTCACTGCCCCAGGCCACGTCGCC 1083
RESULT 8
US-60-360-207-18143
Sequence 18143, Application US/60360207
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
FILE REFERENCE: CL001321
CURRENT APPLICATION NUMBER: US/60/360, 207
CURRENT FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 47235
SEQ ID NO 18143
LENGTH: 1758
TYPE: DNA
ORGANISM: HUMAN
US-60-360-207-18143
Alignment Scores:
Pred. No.: 9.73e-70 Length: 1758
Score: 1250.00 Matches: 224
Percent Similarity: 97.02% Conservative: 4
Best Local Similarity: 95.32% Mismatches: 7
Query Match: 95.42% Indels: 0
DB: 80 Gaps: 0
US-09-847-102A-68 (1-235) x US-60-360-207-18143 (1-1758)
QY 1 MetAlaArgProAspProSerAlaProProSerIleLeuLeuLeuLeuAlaGlnLeu 20
Db 1 ATGGCTGGCTCTGACCCATCCTGGCCGCGCTCTCTGCTGCTGGCTGCGCTG 60
QY 21 ValGlyArgAlaAlaAlaAlaSerLysAlaProValCysGlnGluLeuThrValProMet 40
Db 61 GGGGCCGGGAGCCGCCGGTCAAGGCCAGGGCGCTGCGAGATCACGTTGCCATG 120
QY 41 CysArgGlyLysGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
Db 121 TCCGGCGCATCGCTACACCTGACGACATGCCAACGAGCAACGTCACCATGACCGAG 180
QY 61 AspGluAlaGlyLeuGluAlaHisGlnPheProLeuValGluLeuGlnCysSerPro 80

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Db 181 GACGAGAGCAGGCCTGGAGGCCAACATTGGCCCTTGGAATTCATGCCACCG 240
Qy 81 AspLeuArgPhePheLeuCysThrLeuThrPheLeuProAspTyrIleLys 100
Db 241 GACCTGCCTCTCTGTCGTCTAGTACAGCCATCTTTCCTGACTACCAAG 300
Qy 101 ProSerProProCysArgSerValIleGluArgAlaValAlaGlyCysSerProLeuMet 120
Db 301 CGCGTACACCGTGGCTCGTGTGCGACGGGAGGGGAGCTGGCGCTCATG 360
Qy 121 ArgGlnTrgGlyPheAlaTrpProGluArgNetsSerCysAspArgLeuProValIleGly 140
Db 361 CGCCGATGACCGCTTCCGCGTGTGCGATGACTGGCGCCCTCTGTCATG 420
Qy 141 ArgAspAlaGluIleCysMetAspTYAsnAspSerGlnAlaThrAlaProPro 160
Db 421 GGCGAGCCGAGGTTCTGTGTATGTTATACCGAAGCCACACCGCGTCCC 480
Qy 161 ArgProPheProAlaLysProThrLeuProGlyProGlyAlaProAlaSerGlyGly 180
Db ::::: 481 AAGCTCTCCGGCCAAACCTAACCTCCAGGACCAAGGGGCCATCTCCGGGG 540
Qy 181 GluCysProAlaGlyGlyIleProPheValCysAspCysArgGluProPheValProLeu 200
Db ::::: 541 GAGGCCCCCTGGGAGCCATCCGGAGGAGCTGGAGGAGCTGGGAGCCCTGGC 600
Qy 201 LysGluSerHisProLeuTyrosIysValArgThrglyGlnValProAsnCysAlaLys 220
Db 601 AAGGAGTCACCCACTCTCACACAAAGGTCGCAAGGCCAGTCCAACTGCGGGT 660
Qy 221 ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
Db 661 CCCTCTTACCAAGCCCTCTCAGCCGGACGAGCCACATCGCC 705
Db

RESULT 9
US-60-229-515-1423

; Sequence 1423, Application US/60229515

; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEAR ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000776
; CURRENT APPLICATION NUMBER: US/60/229,515
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 2013
; SOFTWARE: FastSEQ for Windows. Version 4.0
; SEQ ID NO 1423
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: HUMAN
; US-60-229-515-1423

Alignment Scores:
pred. No.: 5.4e-68 Length: 1630
Score: 1222.00 Matches: 217
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.5%
Query Match: 93.28% Mismatches: 0
DB: 66 Indels: 0
Gaps: 0

US-09-847-102A-68 (1-235) x US-60-229-515-1423 (1-1630)

Qy 18 AlagInleuvalGlyArgAlaAlaAlaAlaSerIleAlaProValCysGlnGluIleThr 37
Db 3 GCGCACTGGTGGCCGGCCCGCGTCACAACCTGAGCACATGCCAACAGTCACAC 62
Qy 38 ValProMetCysArgGlyIleGlyIleTyrAsnLeuThrHisMetProAsnGlnPheAlaHis 57
Db 63 GTGCCATGPGCCGGGCACTGGCTACAACCTGAGCACATGCCAACAGTCACAC 122
Qy 58 AspThrGlnAspGluAlaGlyIleGluIvaLHisGlnPheIleProLeuValGluIleGln 77

Db 123 GACCGGGAGGGGGCTGGAGGTCACAGTCCTCCCGCTGGGGATGATCAA 182
Qy 78 CysSerProAspLeuArgPhePheLeuCysThrLeuProAspTyrIleLys 97
Db 183 TCTCTGCGGAACTGCGCTTCCTATGCTATGACACGCCATCTGTCG 242
Qy 98 TyrIleLysProLeuProProCysArgSerValIleGluArgAlaValAlaGlyCysSer 117
Db 243 TACCAAGGAGCTGCGCTGCCCTCGGGAGGCCAGGGCGCTGCG 302
Qy 118 ProLeuMetArgGlnTrgGlyPheAlaTrpProGluArgMetSerCysAspArgLeuPro 137
Db 363 GCTCTGGCCGACGCCGACGCTCTGTCATGAGTAAACAACGCCAGGAGCCAC 422
Qy 158 AlaProProArgProLeuProAlaLysProThrLeuProGlyProGlyAlaProAla 177
Db 423 GGGCCCCAGGCTTCCGCAAGCCACCCCTTCAGGCCAGGGGGGGGGGG 482
Qy 178 SerGlyGlyGlyCysProAlaIleGlyIleProPheValCysAspCysArgGluProPheVal 197
Db 483 TGGGGAGGAGTGGCTGGGCTGGTGGTGGCACTGGCGGAGCCCTGG 542
Qy 198 ProLeuLeuIleGluSerHisProLeuTyrosIlyValArgThrglyGlnValProAsn 217
Db 543 CCCATTGAGGAGTCACACCGCTCTACACAAGGTCGCAAGGCCAGTGCAC 602
Qy 218 CysAlaLysProCysTyrGlyProAspPheSerAlaAspGluArgThrPheAla 235
Db 603 TCGCGGTTACCTGCTTACACAGCCCTCTCACTGCCGACGAGCACGTTGCC 656
Db

RESULT 10
US-60-213-169-11

; Sequence 11, Application US/60213169

; GENERAL INFORMATION:
; APPLICANT: BEASLEY, ELLEN
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEAR ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL00699
; CURRENT APPLICATION NUMBER: US/60/213,169
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 678
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 785
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) .. (785)
; OTHER INFORMATION: n = A,T,C or G
; US-60-213-169-11

Alignment Scores:
pred. No.: 2.87e-57 Length: 785
Score: 1048.00 Matches: 185
Percent Similarity: 95.90% Conservative: 2
Best Local Similarity: 94.87% Mismatches: 8
Query Match: 80.00% Indels: 0
DB: 65 Gaps: 0

US-09-847-102A-68 (1-235) x US-60-213-169-11 (1-785)

Qy 41 CysArgGlyIleGlyIleTyrAsnLeuThrHisMetProAsnGlnPheAlaHis 60
Db 11 TCCAGACTGCGGTTCTACTCTAGAGGACCCCAACCTCAACACGACACCCAG 70
Qy 61 AspGluAlaGlyIleGluIvaLHisGlnPheIleProLeuValGluIleGln 80

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Db          71 GACGCGGGCAGCTTGGGTCACCGGGCCGGCGCGGGAGATCCATGCGCCG 130
Qy          81 AspLeuArgPhePheLeuCysThrMetTyrThrProleuCysLeuProAspTyrHisLys 100
Db          131 GACCTGCCTCTCTCATGCTATGACGCCATCTGCTGCCGACTACCAAG 190
Qy          101 ProLeuProProCysArgSerValCysGluArgAlaLysAlaGlyCysSerProLeuMet 120
Db          191 CGCGTGCAGCCCTGCGCTGGTGCGACGGCCAAAGCGGGGAGCTCCGGCTGGT 250
Qy          121 ArgGlnTyrglypheAlaTrpProLeuArgMetSerCysAspArgLeuProValLeuGly 140
Db          251 CGCCAGTACACTCTCCAGCCAGCGATGACTGCGAACCCGCTCCCGTGTGGC 310
Qy          141 ArgAspAlaGluValLeuCysMetAspTyrAsnGlySerGluAlaThrAlaProPro 160
Db          311 CGCGACGCCGAGGTCTCTGATGATTACACCCAGCGAGGCCACACGGCCCGCCC 370
Qy          161 ArgProPheProAlaLysProThrLeuProGlyProProGlyAlaProAlaSerGly 180
Db          371 AGGCCTTCCAGCCAGCCACCCCTCCAGGCCAGGGCCGGCCCTGGGGG 430
Qy          181 GluGlyProAlaGlyGlyProPheValCysLysCysArgGluProPheValProIleu 200
Db          431 GAATGCCCTGGGAGCCGTTGGGAGGTGGGAGGTGGGAGCTTGACCCATG 490
Qy          201 LysGluSerHisProLeuTyrAsnLysValArgThrGlyGlyValProAsnCysAlaVal 220
Db          491 AAGGAGTCACACCCCTCTCACACAAGTCGGACGGCCAGTCCTCAACTGGCGTA 550
Qy          221 ProCysTyrGlnProSerPheSerAlaAspGluGlyThrPheAla 235
Db          551 CCCTCTTACCGCCCTCTCAGTCGGACGGCACGGTGGCC 595

RESULT 11
US-60-213-170-11
; Sequence 11, Application US/60213170
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, ELLEN
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000699
CURRENT APPLICATION NUMBER: US/60/213,170
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 678
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 785
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) ..(785)
OTHER INFORMATION: n = A,T,C or G
US-60-213-170-11

RESULT 12
US-60-213-169-463
; Sequence 12, Application US/60213169
; General Information:
; Applicant: BEASLEY, ELLEN
; Title of Invention: ISOLATED HUMAN G-PROTEIN COUPLED RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; Title of Invention: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000699
CURRENT APPLICATION NUMBER: US/60/213,169
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 678
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 463
LENGTH: 696
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) ..(696)
OTHER INFORMATION: n = A,T,C or G
US-60-213-169-463

Alignment Scores:
Pred. No.: 2.87e-57 Length: 785
Score: 1048 00 Matches: 185
Percent Similarity: 95.90% Conservative: 2
Best Local Similarity: 94.87% Mismatches: 8
Query Match: 80.00% Indels: 0
DB: 65 Gaps: 0

US-09-847-102A-68 (1-235) x US-60-213-170-11 (1-785)
Qy          41 CysArgGlyIleGlyTyrAspLeuThrHisMetProAspGlnPheAsnHisAspPheGln 60
Db          11 TGCACACTGCGAGGTCTACTCTAGNAGGATCCCCAACAGTTACACACGACCGAG 70
Qy          61 AspGluAlaGlyLeuGluValHisGlnPheTrpProleuValGluIleGlnCysSerPro 80

Db          71 GACGAGCGGGCAGCTTGGGTCACCGGGCCGGCGCGGGAGATCCATGCGCCG 130
Qy          81 AspLeuArgPhePheLeuCysThrMetTyrThrProleuCysLeuProAspTyrHisLys 100
Db          131 GACCTGCCTCTCTCATGCTATGACGCCATCTGCTGCCGACTACCAAG 190
Qy          101 ProLeuProProCysArgSerValCysGluArgAlaLysAlaGlyCysSerProLeuMet 120
Db          191 CGCTCTCCGCTGCGCTCTGTCAGTGGAGCCAGGGCGCTCCGGCTGGT 250
Qy          121 ArgGlnTyrglypheAlaTrpProLeuArgMetSerCysAspArgLeuProValLeuGly 140
Db          251 CGCCAGTACACTCTCCAGCCAGCGATGACTGCGAACCCGCTCCCGTGTGGC 310
Qy          141 ArgAspAlaGluValLeuCysMetAspTyrAsnGlySerGluAlaThrAlaProPro 160
Db          311 CGCGACGCCGAGGTCTCTGATGATTACACCCAGCGAGGCCACACGGCCCGCCC 370
Qy          161 ArgProPheProAlaLysProThrLeuProGlyProProGlyAlaProAlaSerGly 180
Db          371 AGGCCTTCCAGCCAGCCACCCCTCCAGGCCAGGGCCGGCCCTGGGGG 430
Qy          181 GluGlyProAlaGlyGlyProPheValCysLysCysArgGluProPheValProIleu 200
Db          431 GAATGCCCTGGGAGCCGTTGGGAGGTGGGAGGTGGGAGCTTGACCCATG 490
Qy          201 LysGluSerHisProLeuTyrAsnLysValArgThrGlyGlyValProAsnCysAlaVal 220
Db          491 AAGGAGTCACACCCGCTCTCACACAAGTCGGACGGCCAGTCCTCAACTGGCGTA 550
Qy          221 ProCysTyrGlnProSerPheSerAlaAspGluGlyThrPheAla 235
Db          551 CCCTCTTACCGCCCTCTCAGTCGGACGGCACGGTGGCC 595

RESULT 11
US-60-213-170-11
; Sequence 11, Application US/60213170
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, ELLEN
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000699
CURRENT APPLICATION NUMBER: US/60/213,170
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 678
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 785
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) ..(785)
OTHER INFORMATION: n = A,T,C or G
US-60-213-170-11

RESULT 12
US-60-213-169-463
; Sequence 12, Application US/60213169
; General Information:
; Applicant: BEASLEY, ELLEN
; Title of Invention: ISOLATED HUMAN G-PROTEIN COUPLED RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; Title of Invention: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000699
CURRENT APPLICATION NUMBER: US/60/213,169
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 678
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 463
LENGTH: 696
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) ..(696)
OTHER INFORMATION: n = A,T,C or G
US-60-213-169-463

Alignment Scores:
Pred. No.: 3.66e-55 Length: 696
Score: 1014 00 Matches: 178
Percent Similarity: 95.45% Conservative: 2
Best Local Similarity: 98.34% Mismatches: 1
Query Match: 77.40% Indels: 0
DB: 65 Gaps: 0

US-09-847-102A-68 (1-235) x US-60-213-169-463 (1-696)
Qy          55 PheAspHisAspPheGlnAspGluAlaGlyLeuGluValHisGlnPheTrpProleuVal 74
Db          2 TGCACACTGCGAGGTCTACTCTAGNAGGATCCCCAACAGTTACACACGACCGAG 61
Qy          75 GluIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetTyrThrProleu 94

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Db 62 GAGATCCAACTCTCGGGACTGCCCCCTTCATGCCTATGCTATGACCCCCATCTGT 121
 Qy 95 LeuProAspTyrHistylsProLeuProProCysArgSerValCysGluArgAla 114
 Db 122 CTGCCCGACTACCACAGCCGCTGCCCTCCGGCTGGGTGCGAGGCCAAGGCC 181
 Qy 115 GlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAsp 134
 Db 182 GACTGCTCGCCGCTGGCAGTAGCCTTGCCCTGGCCAGGCCATAGCTGGCAC 241
 Qy 135 ArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAspArgSerGlu 154
 Db 242 CGCTCTCCGGCTGGCCGGAGGCTTCCAGGCCAACCTTCAGGCCAGGG 301
 Qy 155 AlaThrThrlAlaProProArgProLeuProLeuProLeuProLeuProGly 174
 Db 302 GCACCAACGGGCCCCCAGGCCCTTCAGGCCAACCTTCAGGCCAGGG 361
 Qy 175 AlaProAlaSerGlyGlyGluCysProAlaGlyGlyProLeuValCysArgGlu 194
 Db 362 GCGCCGCGCTCGGGGGCGAATGCCCGCTGGGCCGTTGTCGAAGTGGCGAG 421
 Qy 195 ProLeuValProLeuLeuGlyGluSerHisProLeuTyrosylsValArgThrGlyGln 214
 Db 422 CCCTCTGTCGCCATTCTGAAGAGTCACCGCTTACACAAGTGCGGAGGCCAG 481
 Qy 215 ValProAsnCysAlaValProCysTyrGlnProSerPheserAlaAspGluArgThrPhe 234
 Db 482 GTGCCCAACTCGGGTACCTGTCTACCGCGTCTCAGGCCAACGCGCAGTC 541
 Qy 235 Ala 235
 Db 542 GCC 544

RESULT 13
 US-60-213-170-463
 ; Sequence 463, Application US/60213170
 ; GENERAL INFORMATION:
 ; APPLICANT: BEASLEY, ELLEN
 ; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
 ; RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
 ; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
 ; CURRENT APPLICATION NUMBER: US/60/213,170
 ; CURRENT FILING DATE: 2000-06-22
 ; NUMBER OF SEQ ID NOS: 678
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 433
 ; LENGTH: 696
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: '(1)..(696)'
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-60-213-170-463

Alignment Scores:
 Pred. No.: 3.66e-55 Length: 696
 Score: 1014.00 Matches: 178
 Percent Similarity: 99.45% Conservative: 2
 Best Local Similarity: 98.34% Mismatches: 1
 Query Match: 77.40% Indels: 0
 DB: 65 Gaps: 0

US-09-847-102A-68 (1-235) x US-60-213-170-463 (1-696)

Qy 55 PheAsnHisAspTyrGlnAspGluLalGluLeuGluValHisGlnPheTrpProLeuVal 74
 Db 2 TMCACACCAGCACGAGGAGAGGCGGCCCTGGAGTGCCTCCAGGGTGGCTGGT 61
 Qy 75 GluIleGlnCysSerProLeuArgPheLeuCysThrMetTyrThrPro 94

Db 62 GAGATCCAACTCTCGGGACTGCCCCCTTCATGCCTATGCTATGACCCCCATCTGT 121
 Qy 95 LeuProAspTyrHistylsProLeuProProCysArgSerValCysGluArgAla 114
 Db 122 CTGCCCGACTACCACAGCCGCTGCCCTCCGGCTGGGTGCGAGGCCAAGGCC 181
 Qy 115 GlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAsp 134
 Db 182 GACTGCTCGCCGCTGGCAGTAGCCTTGCCCTGGCCAGGCCATAGCTGGCAC 241
 Qy 135 ArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAspArgSerGlu 154
 Db 242 CGCTCTCCGGCTGGCCGGAGGCTTCCAGGCCAACCTTCAGGCCAGGG 301
 Qy 155 AlaThrThrlAlaProProArgProLeuProLeuProLeuProGly 174
 Db 302 GCGCCGCGCTGGCCGGAGGCTTCCAGGCCAACCTTCAGGCCAGGG 361
 Qy 175 AlaProAlaSerGlyGlyGluCysProAlaGlyGlyProLeuValCysArgGlu 194
 Db 362 GCGCCGCGCTGGCCGGAGGCTTCCAGGCCAACCTTCAGGCCAGGG 421
 Qy 195 ProLeuValProLeuLeuGlyGluSerHisProLeuTyrosylsValArgThrGlyGln 214
 Db 422 CCCTCTGTCGCCATTCTGAAGAGTCACCGCTTACACAAGTGCGGAGGCCAG 481
 Qy 215 ValProAsnCysAlaValProCysTyrGlnProSerPheserAlaAspGluArgThrPhe 234
 Db 482 GTGCCCAACTCGGGTACCTGTCTACCGCGTCTCAGGCCAACGCGCAGTC 541
 Qy 235 Ala 235
 Db 542 GCC 544

RESULT 14
 US-60-177-646-1336/c
 ; Sequence 1336, Application US/60177646
 ; GENERAL INFORMATION:
 ; APPLICANT: Bonazzi, Vivien
 ; TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: CLO00699
 ; CURRENT APPLICATION NUMBER: US/60/177,646
 ; CURRENT FILING DATE: 2000-01-27
 ; NUMBER OF SEQ ID NOS: 4226
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1336
 ; LENGTH: 611
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 ; US-60-177-646-1336

Alignment Scores:
 Pred. No.: 2.98e-49 Length: 611
 Score: 920.00 Matches: 162
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.39% Mismatches: 0
 Query Match: 70.23% Indels: 0
 DB: 61 Gaps: 0

US-09-847-102A-68 (1-235) x US-60-177-646-1336 (1-611)

Qy 73 LeuValGluIleGlyCysSerProLeuArgPheLeuCysThrMetTyrThrPro 92
 Db 610 CTGGTGGAGATCAAATGCTGGCCGACTCTGGCTTCTCTATGCTACAGGCC 551
 Qy 93 IleCysLeuProAspTyrHistylsProLeuProProCysArgSerValCysGluArgAla 112
 Db 550 ATCTGCTGCCGACTACCAACAGCGCTCCGCCCTGGCTGCGAGGCC 491
 Qy 113 LysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArgMetSer 132

```

Db 490 |||||||AAGGCCGCGCTGCGCCAGTAGGCTTGCGCTGGCCGAGGCATAGC 431
Qy 133 CysAspargleuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAsnArg 152
Db 430 TGTGACCGCCCTCCAGGCTGCTGCCGCGACGCCGAGGTCTTGCGATGATCACCGC 371
Db 153 SerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuProGlyPro 172
Db 370 AGCGAGGCCAACCGGCCGCCAGGCTTCCAGCAAGCCACCTTCAGGCCG 311
Qy 173 ProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyGlyProPheValCysIysCys 192
Db 310 CCAGGSGCGGCGCTGGGGAGGGATGAGGGGCCGCTGCTGCAAGTGT 251
Qy 193 ArgGluProPheValProIleLeuLysGluSerHisProLeuTyrAsnLysValArgThr 212
Db 310 CAGGGGCCGCGCTGGGGCGAAAGCCGCTTGCGAGCAACCCGCTTACACAGGTTGGCAAGTGT 251
Qy 193 ArgGluProPheValProIleLeuLysGluSerHisProLeuTyrAsnLysValArgThr 212
Db 250 CGCAGGCCCTCTGCCCCATTCTGAAAGCTACAGCCGCTTACACAAGTGGCG 191
Db 213 GlyGlnValProAsnCysAlaValProCysTyrGlnProSerPheSerAlaAspGluArg 232
Db 190 GGCAGGCGCCAACTCGCGCTTACCTGCTTACAGCCGCTTACAGGCGACGAGGC 131
Qy 233 ThrPheAla 235
Db 130 ACGTTGCC 122
Db 130 ACGTTGCC 122

RESULT 15
US-60-178-308-1287/C
; Sequence 1287, Application US/60178308

; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000204

; CURRENT APPLICATION NUMBER: US/60/178,308
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 3344
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1287
; LENGTH: 611
; TYPE: DNA
; ORGANISM: HUMAN
; US-60-178-308-1287

Search completed: May 23, 2003, 04:40:15
Job time : 2430 secs

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Alignment Scores:
Pred. No.: 2.98e-49 Length: 611
Score: 920.00 Matches: 162
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.39% Mismatches: 0
Query Match: 70.23% Indels: 0
DB: 61 Gaps: 0

US-09-847-102A-68 (1-235) x US-60-178-308-1287 (1-611)

Qy 73 LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysthrMetTyrThrPro 92
Db 610 CCGTGGAGATCCAATGCTCGCCGACCTGCGCTTCCTCATGCTCTATGACACGCC 551
Qy 93 IleCysLeuProAspTyrHisLysProLeuProProCysAspGlySerValCysGluGala 112
Db 550 ATCTGTCGCCCACTACCAAGCCGCTGCCGCCCTGCCGCTGGTGCAGCGCGCC 491
Qy 113 LysAlaGlyCysSerProLeuMetArgGlnTrgIlyPheAlaTpproGluArgMetSer 132
Db 490 AAGGCCGCGCTGCGCCAGTAGGCTTGCGCTGGCCGAGGCATAGC 431
Qy 133 CysAspargleuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAsnArg 152
Db 430 TGGACGCCCTCCAGGCTGCGCCGCCGAGCTCCCTGCGATGATCACCGC 371
Qy 153 SerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuProGlyPro 172

```

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OM protein - nucleic search, using frame_plus_p2n model.

Run on: May 22, 2003, 18:01:48 ; Search time 603 Seconds

(without alignments)
2021.442 Million cell updates/sec

Title: US-09-847-102A-68
Perfect score: 1310
Sequence: 1 MARPDPSAPPSSLLLIAQL..... PNCAVPCYQPSFSADERTPFA 235

Scoring table: BL05IM62 Xgapext 0.0 Ygapext 0.5 Fgapop 6.0 Fgapext 7.0 Delop 6.0 Delect 7.0

Searched: 6438716 seqs, 2593467500 residues

Total number of hits satisfying chosen parameters: 12877432

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

-DB=USP02/1/USP02_spool/US09847102/runat_19052003_160410_789/app_query.fasta 1.391
-Q=0 -gn2_1/USP02_spool/US09847102/runat_19052003_160410_789/app_query.fasta 1.391
-DB=PENDING_Patents_NA_New -QMT=fastap -SUFFIX=rnpn -MINMATCH=0.1 -LOOPCIR=0
-LOOPEXT=0 -UNITS=bts -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cds.
-LIST=45 -DOALIGN=200 -THR SCORE=100 -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=TCO -NORMEXT
-USER=US09847102 @CGN 1_1_227 @runat_19052003_160410_789 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEE_SCORES -WAIT DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending_Patents_NA_New:*

1: /cgm2_6/prodata/1/pna/PCT NEW COMB seq: *

2: /cgm2_6/prodata/1/pna/US60_NEW_COMB.seq: *

3: /cgm2_6/prodata/1/pna/US07_NEW_COMB.seq: *

4: /cgm2_6/prodata/1/pna/US8_NEW_COMB.seq: *

5: /cgm2_6/prodata/1/pna/US9_NEW_COMB.seq: *

6: /cgm2_6/prodata/1/pna/US9_NEW_COMB.seq2: *

7: /cgm2_6/prodata/1/pna/US9_NEW_COMB.seq3: *

8: /cgm2_6/prodata/1/pna/US10_NEW_COMB.seq: *

9: /cgm2_6/prodata/1/pna/US10_NEW_COMB.seq2: *

10: /cgm2_6/prodata/1/pna/US60_NEW_COMB.seq: *

11: /cgm2_6/prodata/1/pna/US60_NEW_COMB.seq2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1310	100.0	2334	US-10-285-976-48 Sequence 48, Appl
2	1306	99.7	2364	US-10-170-22610 Sequence 22610, A
3	1250	95.4	1758	US-10-144-771-1843 Sequence 18143, A
4	824	62.9	2085	US-10-311-633-18 Sequence 18, Appl
5	824	62.9	3182	US-10-170-23769 Sequence 35769, A
6	824	62.9	3182	US-10-452-680-8744 Sequence 8744, Appl
7	824	62.9	3195	US-10-285-976-54 Sequence 54, Appl

RESULT 1
US-10-285-976-48
Sequence 48, Application US/10285976
GENERAL INFORMATION:
APPLICANT: Rhee, Chae-Seo
APPLICANT: Malini, Sen
APPLICANT: Wu, Christina
APPLICANT: Leoni, Lorenzo M.
APPLICANT: Corri, Maripat
APPLICANT: Carson, Dennis A.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: in Head and Neck Squamous Cell Carcinomas
TITLE OF INVENTION: Frizzled Receptors as Targets for Immunotherapy
FILE REFERENCE: 023070-130320US
CURRENT APPLICATION NUMBER: US10/285, 976
PRIOR APPLICATION NUMBER: US 60/287, 995
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: WO PCT/US02/13802
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 232
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48
LENGTH: 2334
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human frizzled5 (Frz5)
US-10-285-976-48
Alignment Scores:

Pred. No.: 3.17e-80
 Score: 131.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 8

Length: 2334
 Matches: 225
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

DB:

US-09-847-102a-68 (1-235) x US-10-285-976-48 (1-2334)

Qy 1 MetAlaArgProAspProSerAlaProProSerLeuLeuLeuLeuLeuAlaGlnLeu 20
 Db 321 ATGGCTCGCTTCACCCCTCCGCCCTCGTGTGCTGCTGCTGCTGCTGCTG 380
 Qy 21 ValGlyArgAlaAlaAlaAlaSerLysAlaProValCysGlnLeuThrValProMet 40
 Db 381 GGGGCCCCGGCGCCGGCGGCGGCTCAAGGCCCGGTggccAGAAATCACGGTGCCTG 440
 Qy 41 CysArgGlyIleGlyTrasnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
 Db 441 TGGCCGCCATCGCTAACCTGAGCACATGCCAACCGTCACCAACGACACCCAG 500
 Qy 61 AspGluAlaGlyLeuGluValHisGlyProLeuValGluLysGlySerPro 80
 Db 501 GAGGAGGGGGGCGGCTTGAGCTGAGTCCTGCGCTGAGATCCATGCTGCCG 560
 Qy 81 AspLeuArgPhePheLeuCysThrMetThrProLeuCysLeuProAspThrIlys 100
 Db 561 GACCTGGCTCTCTCTCATGACTATGACTATGACAGCCCATCTGCTGCCGACTACCAAG 620
 Qy 101 ProLeuProProCysArgSerValCysGluAlaGlyAlaGlyCysSerProLeuMet 120
 Db 621 CCCTGCGCCCTGGCGCTGGCTGGCGAGCGGCCAGGGCGCTCGCGCGATG 680
 Qy 121 ArgGlnTyrglyPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuAlaGly 140
 Db 681 CGCAGTAGGGCTTGGCTGGCCCTCCGGCTGGCG 740
 Qy 141 ArgAspAlaGluValLeuCysMetAspThrAsnArgSerGluAlaThrAlaProPro 160
 Db 741 CGCGACGCCGAGTCCTCTGATGATTACACCGAGCGGCCACCGGCC 800
 Qy 161 ArgProProProAlaLysProThrLeuProGlyProProGlyAlaProAlaSerGly 180
 Db 801 AGCCCTTCCCAGCCAGCCACCTTCAGGCCAGGGCGCC 860
 Qy 181 GLUCYSProAlaGlyGlyProLeuValCysLysCysArgGluProLeuValProLeu 200
 Db 861 GAAATGCCCGCTGGGGGCCGTTGGTGCAGTGTCCGGAGGCCCTCGTGCCCATCTG 920
 Qy 201 LysGluSerHisProLeuTyrasnLysValArgThrGlyGlnValProAsnCysAlaVal 220
 Db 921 AAGGGTCAACCCGCTCATCACAAAGTGCGGAGGCCAGCTGCCCAACTGGCGGT 980
 Qy 221 ProCysTyrgInProSerPheserAlaAspGluArgThrPheAla 235
 Db 981 CCCGTGCTAACCGCAGCTCTAGGCCGAGGCCAGTCGCC 1025

RESULT 2

US-10-170-235-22610
 ; Sequence 22610, Application US/10170235

; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig
 ; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
 ; FILE REFERENCE: CL001380
 ; CURRENT APPLICATION NUMBER: US/10/170-235
 ; CURRENT FILING DATE: 2003-03-17
 ; NUMBER OF SEQ ID NOS: 42514
 ; SEQ ID NO: 22610
 ; LENGTH: 2674
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 US-10-170-235-22610

US-09-847-102a-68 (1-235) x US-10-170-235-22610 (1-2674)

Alignment Scores:
 Pred. No.: 6.94e-80
 Score: 1306.00
 Percent Similarity: 100.00%
 Best Local Similarity: 99.57%
 Query Match: 8
 Gaps: 0

Length: 2674
 Matches: 234
 Conservative: 1
 Mismatches: 0
 Indels: 0

DB:

US-09-847-102a-68 (1-235) x US-10-170-235-22610 (1-2674)

Qy 1 MetAlaArgProAspProSerAlaProProSerLeuLeuLeuLeuLeuAlaGlnLeu 20
 Db 482 ATGGCTGGCTGACCCATGCCGCCGCCCTCGCTGTGCTGCTCTGCGAGCTG 541
 Qy 21 ValGlyArgAlaAlaAlaAlaSerLysAlaProValCysGlnLeuThrValProMet 40
 Db 602 TGCCGGCATGGGTACAACCTGAGCACATGCCACACAGTCACACGACACGAG 661
 Qy 61 AspGluAlaGlyLeuGluValHisGlnPheTrProLeuValGluLeuGlySerPro 80
 Db 662 GAGGAGGGGGCTGGAGGACCGAGTCGGGGCTGGGGAGATCAAATGCGCG 721
 Qy 81 AspLeuArgPhePheLeuCysThrMetThrProLeuCysLeuProAspThrIlys 100
 Db 722 GACCTGGCTCTCTCATGCTCTGCTGAGTCAGGCCATCTGCTGCCGACTACACAG 781
 Qy 101 ProLeuProProCysArgSerValCysGluArgAlaGlyCysSerProLeuMet 120
 Db 782 CGCGTCGCCCTGGCCCTGGCTGGGGCTGGAGGCCACGGCGCTGCGCGCTGATG 841
 Qy 121 ArgGlnTyrglyPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuAlaGly 140
 Db 842 CCACATGAGCTTCCCTGGCCGAGGGATGACTGGCCCTCCGGTGTGGC 901
 Qy 141 ArgAspAlaGluValLeuCysMetAspThrAsnArgSerGluAlaThrAlaProPro 160
 Db 902 CGCGAGGCCAGGGCTCTGATGGATTACACCGAGGCCAGGCCACAGGGGCC 961
 Qy 161 ArgProProProAlaLysProThrLeuProGlyProProGlyAlaProAlaSerGly 180
 Db 962 AGGCCTTCCCAGCCAGCCACCCCTCCAGGGGCCAGGGGCCCTGGGG 1021
 Qy 181 GLUCYSProAlaGlyGlyProLeuValCysLysCysArgGluProLeuValProLeu 200
 Db 1022 GAATGCCCGCTGGGGCCCTGGTGTGAAAGTCGGCCAGGCCCTTGRCCT 1081
 Qy 201 LysGluSerHisProLeuTyrasnLysValArgThrGlyGlnValProAsnCysAlaVal 220
 Db 1082 AAGGGTCAACCCGCTCATCACAAAGTGCGGAGGCCAGTCGCC 1141
 Qy 221 ProCysTyrgInProSerPheserAlaAspGluArgThrPheAla 235
 Db 1142 CCCGTGCTAACCGCAGCTCTAGGCCGAGGCCAATGCGCGTA 1186

RESULT 3

US-10-144-771-18143
 ; Sequence 18143, Application US/10144771

; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig
 ; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
 ; FILE REFERENCE: CL001321
 ; CURRENT APPLICATION NUMBER: US/10/144-771
 ; CURRENT FILING DATE: 2003-05-15
 ; NUMBER OF SEQ ID NOS: 47235
 ; SEQ ID NO: 18143
 ; LENGTH: 1758
 ; TYPE: DNA
 ; ORGANISM: HUMAN

US-10-144-771-18142

Alignment Scores:
 red. No.: 2.94e-76
 core: 1250.00
 Average Similarity: 97.028
 Lowest Local Similarity: 95.328
 Every Match: 95.428

APPLICANT: DING, Li; SANJUANWALA, Makansubu
APPLICANT: DUGGAN, Brenda M.; LU, Yam
TITLE OF INVENTION: RECEPTORS
FILE REFERENCE: PP-0793 USN
CURRENT APPLICATION NUMBER: US/10/311,623
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US 01/19942
PRIOR FILING DATE: 2001-06-21

; OTHER INFORMATION: Incyte ID No: 153444CBI
US-10-311-623-18

Alignment:	Scores:	5.24e-47	Length:	2095
Pred. No.:			Matches:	161
Score:	824.00		Conservative:	21
Percent. Similarity:	67.65%		Mismatches:	39
Best Local Similarity:	59.85%		Indels:	48
Query Match:	62.90%		Gaps:	8
DB:	9			

Qy	11	SerLeuLeu-----LeuLeuLeuLeuLagLnuEuaValGlyArgAlaAlaAlaLaser	28
Db	31	TCCGTGCGGCCCTTGCGCCTGTCAGCGCCTAGCGGGCTGC GGCCCGCCCTGGCC	90
Qy	29	LysalaProValGlyGlnLuiLeuThrValProMetCysArgGlyYlglGLYRanleu	48
Db	91	AAGGAGCTGCATGCCAAGAGATCACCGCCGCTGTAAGGCCATCGCTAACACTAC	150
Qy	49	ThrHisMetProIasnGlnPheAsnHisIaspThrGlnAspGluAlaGlyLeuGluValHis	68
Db	151	ACTTACATGCCAAATCACTTCAACCACGACACCAGAGGGCCCTGGAGCTGGCAC	210
Qy	69	GlnGlyHtpProLeuValGluLleGlyCysSerProAspLeuArgPhePheLeuYsThr	88
Db	211	CAGTCCTGGCCGCTGIGGAGATTCAGTCAGTCGCTGCCGATCTCAGTCCTCTCTGTCAGC	270
Qy	89	MetTrpThrProLeuProAspThrHisAspProLeuProProCysSerVal	108
Db	271	ATGTCACGCCCATCTGCTTAGAGGACTACAAGAGAGCCCTGCCCCGGCGCGCG	330
Qy	109	CysGluLArgAlaLysAlaGlyCysSerProLeuMetAspGlnTyg1PheAlaTrpPro	128
Db	331	TGGAGGCCGCCAGGCCGCTCGCGCGCTATGCCAGAGGCCCTCGCTGGCC	390
Qy	129	GluArgMetSerCysBspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMet	148
Db	391	GACCGATGCGCTGCCGACCGGCTGCGCCAGCAAGGC--AACCTGACACGCCGCTGCGATG	447
Qy	149	AspTYrAsnArgSerGluLalathrThrala-----ProProAspProProProAla	165
Db	448	GACTAACCCGACGCCGCTAACCAACCCGACCCAGCCGCCGCGCCGCTGCC	507
Qy	166	LysProTrpLysLeuProGly-----ProGly-----ProGly	174
Db	508	CCGGCG-----CCGGCGAGGCCGCTTCGGCAGGGCCAGGGCCACGGCCACCGGG	561

APPLICANT: Ren, Feiyan
 APPLICANT: Xue, Rideng J.
 APPLICANT: Wang, Jian-Rui
 APPLICANT: Wehrman, Tom
 APPLICANT: Ghosh, Malabika
 APPLICANT: Wang, Dunrui
 APPLICANT: Zhao, Qing A.
 APPLICANT: Wang, Zhiwei
 TITLE OF INVENTION: Novel Nucleic Acids and
 TITLE OF INVENTION: Secreted Polypeptides
 FILE REFERENCE: 805ACON
 CURRENT APPLICATION NUMBER: US/10/112, 944
 CURRENT FILING DATE: 2002-04-30
 PRIOR APPLICATION NUMBER: US 10/112, 944
 PRIOR FILING DATE: 2002-03-28
 PRIOR APPLICATION NUMBER: US 60/306, 971
 PRIOR FILING DATE: 2001-07-21
 PRIOR APPLICATION NUMBER: US 09/488, 725
 PRIOR FILING DATE: 2000-01-21
 PRIOR APPLICATION NUMBER: US 09/491, 404
 PRIOR FILING DATE: 2000-01-25
 PRIOR APPLICATION NUMBER: US 09/496, 914
 PRIOR FILING DATE: 2000-02-03
 PRIOR APPLICATION NUMBER: US 09/515, 126
 PRIOR FILING DATE: 2000-02-28
 PRIOR APPLICATION NUMBER: US 09/519, 705
 PRIOR FILING DATE: 2000-03-07
 PRIOR APPLICATION NUMBER: US 09/540, 217
 PRIOR FILING DATE: 2000-03-31
 PRIOR APPLICATION NUMBER: US 09/552, 929
 PRIOR FILING DATE: 2000-04-18
 PRIOR APPLICATION NUMBER: US 09/577, 408
 PRIOR FILING DATE: 2000-05-18
 NUMBER OF SEQ ID NOS: 924
 SOFTWARE: pt_FL_genes Version 5.0
 SEQ ID NO: 6
 LENGTH: 3206
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE: CDS
 NAME/KEY: CDS
 LOCATION: (381)..(2462)
 S-10-115-678-6

ALIGNMENT SCORES:
 red. No.: 8.53e-47 Length: 3206
 core: 824.00 Matches: 161
 percent Similarity: 67.66% Conservative: 21
 best Local Similarity: 59.85% Mismatches: 39
 query Match: 62.90% Indels: 48
 B: Gaps: 8

RESULT⁹
 US-10-112-944-6
 ; Sequence 6, Application US/10112944
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Weng, Gehui
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Xue, Rideng J.
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Ghosh, Malabika
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Wang, Zhiwei
 TITLE OF INVENTION: Novel Nucleic Acids and
 TITLE OF INVENTION: Secreted Polypeptides
 FILE REFERENCE: 805A
 CURRENT APPLICATION NUMBER: US/10/112, 944
 CURRENT FILING DATE: 2002-03-28
 PRIOR APPLICATION NUMBER: US 09/488, 725
 PRIOR FILING DATE: 2000-01-21
 PRIOR APPLICATION NUMBER: US 09/491, 404
 PRIOR FILING DATE: 2000-01-25
 PRIOR APPLICATION NUMBER: US 09/496, 914
 PRIOR FILING DATE: 2000-02-03
 PRIOR APPLICATION NUMBER: US 09/515, 126
 PRIOR FILING DATE: 2000-02-28
 PRIOR APPLICATION NUMBER: US 09/519, 705
 PRIOR FILING DATE: 2000-03-07
 PRIOR APPLICATION NUMBER: US 09/540, 217
 PRIOR FILING DATE: 2000-03-31
 PRIOR APPLICATION NUMBER: US 09/552, 929
 PRIOR FILING DATE: 2000-04-18
 PRIOR APPLICATION NUMBER: US 09/577, 408

109 CysGluGalaLysAlaGlyCysSerProLeuMetArgGlnTrpGlyPheAlaPro 128
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 711 TCGAGAGCCAAAGGCCGCTGGCGCTCTAGGCCGAGTCGCTTGCCTGGCCC 770
 129 GluArgMetSerCysAspArgLeuProValLeuGlyArgAlaGluValLeuCysMet 148
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 771 GACCGATGCCCTGGACCGCTGCCGACAGCAAGGC--AACCTGACAGCTGCTGATG 827
 149 AspTyrAsnArgSerGluAlaThrThrAla-----ProProArgProProAla 165
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 828 GACTACAACCGCACCGACCTAACACCGCCGCGCCAGCCGCCCCCTGCGCCCG 887
 166 LysProThrIleProGlu-----ProProGly 174
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 888 CGCGCG-----CCGGCGAGCAAGCAAGCGCTTCGGCAGGGCCACGGCCCGCC 941
 Qy 175 Ala----- 175
 |||||
 942 GCCAGCCCCGACCCGGCGAGGGCGCTGGCGGGGAGCGGGCGCCGGCGCC 1001
 Qy 176 ProAlaSerCysGly-----GluCysProAlaGlyGlyProProVal 189
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1002 CCAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCCC 1051
 Qy 190 -----CysLysCysBarGluGluProProAlaProLeuLysLysSerHisPro 205
 ||||| ||||| :::: ||||| ||||| ||||| ||||| ||||| |||||
 Db 1062 TGGAGGCCGGTGCGAGCTGCCGCGCTATGGAGGGTGTAGCCGAGGCCACCG 1121
 Qy 206 LeuTyRAsnLysValArgTrgGlyLysValProAsnCysAlaValProCysTyrcInPro 225
 ||||| ||||| :::: ||||| ||||| ||||| :::: ||||| ||||| :::: |||||
 Db 1122 CTCTACAAACCGCTAACAGAGCTGAGTAAGCTGCTACTGCCGCTGCCACACCC 1181
 Qy 226 SerProSerAlaArgGluArgThrPhe 234
 ||||| ||||| ||||| ||||| ||||| |||||
 Db 1182 TTTTCAGCCAGGAGCGCGCCCTC 1208

PRIOR FILING DATE: 2000-05-18
 NUMBER OF SEQ ID NOS: 924
 SOFTWARE: pt_FL_genes Version 5.0
 SEQ ID NO: 6
 LENGTH: 3206
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE: CDS
 LOCATION: (381)..(2462)
 US-10-112-944-6

Alignment Scores:
 Pred. No.: 8.53e-47
 Score: 824.00
 Percent Similarity: 67.66%
 Best Local Similarity: 59.85%
 Query Match: 62.90%
 DB: 8

length: 3206
 matches: 161
 conservative: 21
 mismatches: 39
 indels: 48
 gaps: 8

US-09-847-102A-68 (1-235) x US-10-112-944-6 (1-3206)

Qy 11 SerLeuLeu----LeuLeuLeuLeuAlaGlnLeuValGlyArgAlaAlaAlaLaser 28
 Db 411 TCGCTGCTGGCGCCCTGGCTTGCGCTGCGCAGGCCCTAGCGCGCTCGGGCTGGCC 470
 Qy 29 LysAlaProValCysGlnGluLeuValProMetCysArglyIleGlyTyrAlaLeu 48
 Db 471 AGGAGCTGGATGCCAGAGATCACCGTCGGCTGTGAAGGCATCGGTACAATAC 530

Qy 49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluAlaHis 68
 Db 531 ACCTACATGCCCCATCAGTTTACCAAGAACGAGAACGAGGCGCCCTGGAGGTGAC 590
 Qy 69 GlnPheTrpProLeuValGluLeuGlnCysSerProAspLeuArgPhePheLeuCysThr 88
 Db 591 CAGTTCTGGCCCTGGAGAATCCAGTCAGTCTCGCTGCGCCATCTCAAGTCTCTGTCAGC 650
 Qy 89 MetTYrThrProLeuValProAspProAspLeuProProCysArglyIleGlyTyrAlaLeu 108
 Db 651 ATGTAACCGCCATCTCTAGAGGACTACAGAAAGCCGCTGCCGCTGCGCTGGTG 710

Qy 109 CysGluArgAlaLysAlaGlyCysSerProLeuMetArgGlnTyrglyPhalaTtPro 128
 Db 711 TCGGAGGGCGCCAGGGCGCTGGCGCCGTCATGGCCAGTCACGCTTGCGCTGGCC 770

Qy 129 GluArgMetSerCysAspArgLeuProValLeuGlyArgAlaGluValLeuCysThr 148
 Db 771 GACCGCATGCCCTGCGAACCGCTGCCGAGGAGGAC---AACCTGACACCGCTGTCATG 827

Qy 149 AspTYrAsnArgSerGluAlaThrThrAla-----ProProArgProPheProAla 165
 Db 828 GACTACACCCACCGACCTAACACGCCGCCAGGCCACGCCACGCCCTGGCGCCG 887

Qy 166 LysProThrLeuProGly-----ProProGly 174
 Db 888 CGCCG-----CCGGGAGCAGCCCTTGGGAGGCCACGCCGCCCCGGGG 941

Qy 175 Ala-----175

Db 942 GTCAGGCCCTCACCGCGCGCAGGGCGGGAGGGAGCGGGGGAGCGGGGGAGCCC 1001

Qy 176 ProAlaSerGlyGly-----GluCysProAlaGlyGlyProPheVal 189

Db 1002 CGACGCTGGCGCGCCGCGGGAGGGGGCCCTGGCGGGAGGGGGAGGGGGCTGCC 1061

Qy 190 -----CysLysCysArgGluProPheValProLeuLysGluSerHisPro 205
 Db 1062 TCGGAGGCCGGGGTGGCTGGCGCCCTTGGTGGCTGCCACGGCCACCCG 1121

Qy 206 LeuTYrAsnLysValArgThrGlyGlyInValProAspCysAlaValProCysTyrglyPro 225
 Db 1122 CTCTACACCCTGTCAGACAGGCCAGTCCTAACTGCGCTGCGCTGCCACACCCC 1181

Qy 226 SerPheSerAlaAspGluArgThrPhe 234
 Db 1182 TTTTCAGCCAGGAGGCCGCCCTTC 1208

RESULT 10

Sequence 10276, Application US/10144771
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig
 TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
 FILE REFERENCE: CL001321
 CURRENT APPLICATION NUMBER: US10/144,771
 CURRENT FILING DATE: 2002-05-15
 NUMBER OF SEQ ID NOS: 47235
 SEQ ID NO: 10276
 LENGTH: 2058
 TYPE: DNA
 ORGANISM: HUMAN
 US-10-144-771-10276

Alignment Scores:
 Pred. No.: 5.58e-47
 Score: 823.50
 Percent Similarity: 69.06%
 Best Local Similarity: 60.00%
 Query Match: 62.86%
 DB: 9

length: 2058
 matches: 159
 conservative: 24
 mismatches: 39
 indels: 43
 gaps: 8

US-09-847-102A-68 (1-235) x US-10-144-771-10276 (1-2058)

Qy 11 SerLeuLeu----LeuLeuLeuLeuAlaGlnLeuValGlyArgAlaAlaAlaLaser 28
 Db 31 TCGCTCTTAACGCCCTGGCGCTGCTACAGGCTCTAGCGCGCTGCCCGGCTTGCGC 90

Qy 29 LysAlaProValCysGlnGluLeuValProMetCysArglyIleGlyTyrAlaLeu 48
 Db 91 AGGAGCTGGGTGCCAGAGATCACGGCTGGTGCAGGGCTGGTACAATAC 150

Qy 49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluAlaHis 68
 Db 151 ACTTACATGCCAACCGTCACAGTCAGGACAGGATAGGGGGCTAGAGGTGAC 210

Qy 69 GlnPheTrpProLeuValGluLeuGlnCysSerProAspLeuArgPhePheLeuCysThr 88
 Db 211 CAGTTTGGCGCTGGGGAGATACTGTCCTCCGGACTCTAGTTCTCTGTCAG 270

Qy 89 MetTYrThrProLeuCysLeuProAspProAspTYrHisLysProLeuProProCysArgSerVal 108
 Db 271 ATGTAACGCCATCTGCCCTGGAGGACTACAGAAAGCCCTGCGCCCTTGCGCTGTG 330

Qy 109 CysGluArgAlaLysAlaGlyCysSerProLeuMetArgGlnTyrglyPhalaTtPro 128
 Db 331 TGTGACGCCAACGCCCTGCGCCCTCATGGCGCTGAGGTGCTTGCGCT 390

Qy 129 GluArgMetSerCysAspArgLeuProValLeuGlyArgAlaGluValLeuCysMet 148
 Db 391 GACCGCATGCCCTGGCGCTGCTGGTGGCTGCCACCCGAGGAC---AACCCGAGACTCTGTCATG 447

Qy 149 AspTYrAsnArgSerGluAlaThrThrAla-----ProProArgProPheProAla 165
 Db 448 GACTACACCCACCGACTCACCAGGCCGCCAGGCCACGCCGCCCTGCGCTCG 507

Qy 166 LysProThrLeuProGly-----ProProGly 174
 Db 508 CGCGCTCTCT---CCGGGAGCAGCGCCCTCTGGAGGCCACGCCGCCGCGAGGG 564

Qy 175 Ala-----175

Db 565 GCCAGCCCCACATCTGGGGCGAGGAGGGACGGGGAGGGCTGCC 624

Qy 176 ProAlaSerGlyGlyGluCys-----ProAlaGlyGlyProPheVal-----189

Db 625 CCTCTGCCGCCGGGAGGCCCCCTGatggccgcgtctccgtggagg 684
 Qy 190 CyblyscysarargluProPheValProleuIysGluSerIisProLeuTyRasIys 209
 Db 685 TGCAGTCGCCGCCATGGTGCCAGGCCACCGCTCTAACCGC 744
 Qy 210 ValArgThrArgLysValProAlaProCysTyrGlnProSerResAla 229
 Db 745 GTCAAGACGCCAGATGCCAACTGTGCGCTGCCCTCACACCCCTTTAGCCAG 804
 Qy 230 AspGluArgThrLe 234
 Db 805 GATGAGGCCGCCCTTC 819

RESULT 11
 US-10-144-771-12343
 ; Sequence 12343, Application US/10144771
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig
 ; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
 ; FILE REFERENCE: C1001321
 ; CURRENT APPLICATION NUMBER: US/10/144,771
 ; NUMBER OF SEQ ID NOS: 47235
 ; SEQ ID NO 12343
 ; LENGTH: 2043
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 ; US-10-144-771-12343

Alignment Scores:
 Pred. No.: 1.97e-23
 Score: 419.50
 Percent Similarity: 54.05%
 Best Local Similarity: 42.47%
 Query Match: 36.60%
 DB: 9 Gaps: 11

Length: 2043
 Matches: 110
 Conservative: 30
 Mismatches: 79
 Indexes: 40

US-09-847-102A-68 (1-235) x US-10-144-771-12343 (1-2043)

Qy 3 ArgProAspProSerAlaPro-ProSeLeuLeuLeu---LeuLeuLeuAlaGlnLeuVa 21
 Db 217 CGCCCTGCCGCCGAGGCCCTGCCGCCCTGCTGCTGCTGCTGCTGCTGCTGCCGCC 276
 Qy 21 IGLYArgAlaAlaAlaAlaAlaSerIysAlaProVal-----CysGln 34
 Db 277 CGACGCCCACTTCCACGGGAGAGCGCATCCCGGACGCGCTCTGCCA 336
 Qy 34 nGluIleThrValProMetCysArgLysIleGlyTYrasIleThrValMetProAsnG1 54
 Db 337 GCCCATCTCCATCCCGCTGCAAGGACATCGCTCACACAGACCTCATGCCAACCT 396
 Qy 54 nPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpProLeuVa 74
 Db 397 TCTTGCCACACGAACAGGAAGACCGGGCCCTGGAGGTGCACTGAGTTCTACCGCTGGT 456
 Qy 74 IGLuIleGlnCysSerProAspLeuAspIleLeuCysThrMetTyRhtProLeu 94
 Db 457 GAAGGTGCTGCTGCTGCCGAGCTGCGCTCTCTGCTCATGAGCGCCGCGT 516
 Qy 94 SLeuProAspTyRhiLysProLeuProProCysAspSerValCysGluAlaAlaLysAla 114
 Db 517 CACAGTG---CTGCAGCAGGCCATCCCGCCGAGCCGCTCCATCTGCGAGGCCGCCA 573
 Qy 114 aglyCysSerProLeuMetArgLysValTyRhtPheAlaLrpProGluAlaGmeSerCys 134
 Db 574 AGGCTGCAGGCCCTCATGAGCAAGTGTCCAAATGGCCGGCCCTCGCTGCGA 633
 Qy 134 pargleuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyRhiLysArgSerG1 154
 Db 634 GCATTCCGCCGCTCACGCC-----GCGAGCAGATCTGCGCTGCCAGAACCTCTG 687
 Qy 154 u-----AlaThrThAlaProProArgProProLeuAlaLysProTh 168

RESULT 12
 US-10-285-976-42
 ; Sequence 42, Application US/10285976
 ; GENERAL INFORMATION:
 ; APPLICANT: Rhee, Chae-Seo
 ; APPLICANT: Malin, Sen
 ; APPLICANT: Wu, Christina
 ; APPLICANT: Leon, Lorenzo M.
 ; APPLICANT: Corr, Maripat
 ; APPLICANT: Carson, Dennis A.
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
 ; FILE REFERENCE: 023070-13020US
 ; CURRENT APPLICATION NUMBER: US/10/285, 976
 ; CURRENT FILING DATE: 2002-11-01
 ; PRIORITY APPLICATION NUMBER: US 60/287, 995
 ; PRIORITY FILING DATE: 2001-05-01
 ; PRIORITY APPLICATION NUMBER: WO PCT/US02/13802
 ; PRIORITY FILING DATE: 2002-05-01
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 42
 ; LENGTH: 1983
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human frizzled2 (Fz2d2)
 ; US-10-285-976-42

Alignment Scores:
 Pred. No.: 2.83e-23
 Score: 477.00
 Percent Similarity: 53.70%
 Best Local Similarity: 41.63%
 Query Match: 36.41%
 DB: 8 Gaps: 10

Length: 1983
 Matches: 107
 Conservative: 31
 Mismatches: 81
 Indexes: 38
 Gaps: 10

US-09-847-102A-68 (1-235) x US-10-285-976-42 (1-1983)

Qy 3 ArgProAspProSerAlaProProSerLeuLeuLeuLeuLeuAlaGlnLeuValGly 22
 Db 136 CGGCCGCCAGGCCCTGCCGCCCTGCTGCGCTGCTGCCGCCGCC 195
 Qy 23 ArgAlaAlaAlaAlaSerIysAlaProVal-----CysGlnGlu 35
 Db 196 CGGGCCAGTTCACGGGAGAGGCCATCTCATCCGGACACCGCTCTGCCAGCC 255
 Qy 36 IleThrValProMetCysArgLysIleGlyTyRhiLysAspLeuThrHiMetProAsnG1nPhe 55
 Db 256 ATCTCCATCCCGCTGCGACAGCATGCCACCATCATGCCAACCTCTG 315
 Qy 56 AsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGlu 75

Db 316 GCGCACACGAAACCAGAGGAGCCAGGCCTAGAGGTCTATCCCTGGTGAAG 375
 Qy 76 IleGlnCysSerProAspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeu 95
 Db 376 GTGCACTGCTGCCGAACTGGCTCTCTGTGTCATGTCACGCCACCGTGAC 435
 Qy 96 ProAspTyrHisLysProLeuProProCysBargSerValCysGluArgAlaLysAlaLys 115
 Db 436 GTG--CTGGAACAGGCCATCCGCCGCTGCCCTCATCTGAGGCCAGGCC 492
 Qy 116 CysSerProLumetArgGlnTyrglyPheAlaTrpProGluArgMetSerCysPasparg 135
 Db 493 TCGGAAGGCCCTCATGAAACAGCTGGTTAGTGGCCGGGCGGCCGAGCAC 552
 Qy 136 LeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAsnArgSerGlu-- 154
 Db 553 TTCCCGGCCAGGC---GCCGACAGCTGCTGCCAGAACCTCCGAGAC 606
 Qy 170 ProGlyProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyGly-- 186
 Db 661 GGGGACCCCCGGTGGCCGGGGGGCGCCGCTACGCCACGGCGAG 720
 Qy 187 --ProPheValCysLysCysArgGluProPheValProIleLeuGlyGluSerHisPro 205
 Db 721 CACCCCTTCGCTGCCG---CGCGCTCAGGCG---CCA 756
 Qy 206 LeuTyRAsnLySValGlyGlyGlnValProAspCysAlaValProCysTyrglnPro 225
 Db 757 TCCTATCTCAGCTACAGTTCTGGCGAGGCTGATGTCGCGCCCTGC--GAACCT 813
 Qy 226 Ser-----PheSerAlaAspGluArgThrHeAla 235
 Db 814 GCGCGCCCGATGGTTCATGTTCTCACAGGAGGAGCGGTTTCGG 864

RESULT 13
 US-0-225-567A-381
 ; Sequence 381, Application US/10225567A
 ; GENERAL INFORMATION:
 ; APPLICANT: LifeSpan Biosciences
 ; APPLICANT: Brown, Joseph P.
 ; APPLICANT: Burmer, Glenna C.
 ; APPLICANT: Roush, Christine L.
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 1920-A-4
 ; CURRENT APPLICATION NUMBER: US/10/225,567A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,144
 ; NUMBER OF SEQ ID NOS: 2292
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 381
 ; LENGTH: 1983
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-225-567A-381

Alignment Scores:
 Pred No.: 2.83e-23 Length: 1983
 Score: 477.00 Matches: 107
 Percent Similarity: 53.70% Conservative: 31
 Best Local Similarity: 41.63% Mismatches: 81
 Query Match: 36.41% Indels: 38
 DB: 9 Gaps: 10

RESULT 14
 US-10-170-235-33965
 ; Sequence 33965, Application US/10170235
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig
 ; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
 ; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
 ; FILE REFERENCE: CI001380
 ; CURRENT APPLICATION NUMBER: US/10/170,235
 ; CURRENT FILING DATE: 2003-03-17
 ; NUMBER OF SEQ ID NOS: 42514
 ; SEQ ID NO 33965
 ; LENGTH: 1933
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 ; US-10-170-235-33965

Alignment Scores:
 Pred No.: 5.58e-23 Length: 1933
 Score: 472.50 Matches: 108
 Percent Similarity: 54.33% Conservative: 30
 Best Local Similarity: 42.52% Mismatches: 77
 Query Match: 36.07% Indels: 39
 DB: 8 Gaps: 11

US-09-847-102A-68 (1-235) x US-10-170-235-33965 (1-1933)

Alignment Scores:

102

freq. No.:	5,386-23	Batches:	1935
Score:	472.50	Conservative:	108
Percent Similarity:	54.33%	Mismatches:	77
Best Local Similarity:	42.52%	Indices:	39
Query Match:	36.07%	Gaps:	11
DB:	11		

Db 67 TTCCACCGGAGAGGCCATCCCTCATCCCGGACCAAGCTTCAGCCCATCTCCATC :::::
 Qy 39 ProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetProLysGlnPheAsnHsAsp 58
 Db 127 CGCTCTCACGGACATGCCTAACAGACCATATGCCAACACTCTGGCCACG 186
 Qy 59 ThrglnAspGluAlaGlyIleGluValHisGlnPheTrpProLeuValGluIleGlyCys 78
 Db 187 AACCGAGGACGGCTAGAGGTGACACTCTAACCGTGTCAGAGGTGAGSTG 246
 Qy 79 SerProAspLeuArgPhePheLeuCysThrMetThrProLeuCysLeuAspTyr 98
 Db 247 TCGCCCGAACTGCCTTCPTCCTGTCATGTCACCCGTGTCACCGTG 303
 Qy 99 HisLysProLeuProProCysArgSerValCysGluValGalaLysAlaGlyCysSerPro 118
 Db 304 GACACGGCCATCCGGCCGCTCTATCTGAGCCGGGGCAGGGCTCGAAGCC 363
 Qy 119 LeuMetArgGlnIrrglyPheAlaTrpProGluArgMetSerCysAspArgLeuProVal 138
 Db 364 CTCATGACAAGTGGTTTCAGTGGCCGAGGCCCTGGCTGGAGCACCTCCCGC 423
 Qy 139 LeuGlyArgAspAlaGluValLeuCysMetAspTyrosArgSerGlu----- 154
 Db 424 CACGGC-----GCGCAGCAGATCTGGCTGGCCAGAACACTCCGAGGACGCTGCC 477
 Qy 155 -----AlaThrThrAlaProProArgPropeProAlaLysProThrLeuProGlyPro 172
 Db 478 GCCTACTCTCACCCACCCCCGCCCCGGCGGACTG-----CAGCGGTTGCCGGGGGACC 531
 Qy 173 ProGlyAlaProAlaSerArgGlyGlyGlyLucysProAlaIgLy-----Prope 188
 Db 532 CCGGTGCCCCGGCCCCGGCTCCCCCGCTACGCCACGCTGGAGCACCCCTTC 591
 Qy 189 ValCysLysCysArgGluProProValProLeuLysGluSerHisProLeuTyraAsn 208
 Db 592 CACTGCCG-----CGCTCCTCAAGGTG-----CCATCCTATCTC 627
 Qy 209 LysValIargThrGlyGlnValProAsnCysAlaValProCysTyrGlnProSer---- 226
 Db 628 AGCTTACAAGTTCTGGCGAGGCTGATGTCGTCGCGGCCCTGC--GAACCTGGCGGCC 684
 Qy 227 -----PhesAlaAspGluIargThrPheAla 235
 Db 685 GATGGTTCCATGTCTCACAGGAGGACGGTTGCGC 726

RESULT 15

US-60-453-135-1905

Sequence 1905, Application US/60453135

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele

APPLICANT: IAKUBOVA, Olga

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001456

CURRENT APPLICATION NUMBER: US/60/453,135

CURRENT FILING DATE: 2003-03-10

NUMBER OF SEQ ID NOS: 82762

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1905

LENGTH: 1933

TYPE: DNA

ORGANISM: Homo sapiens